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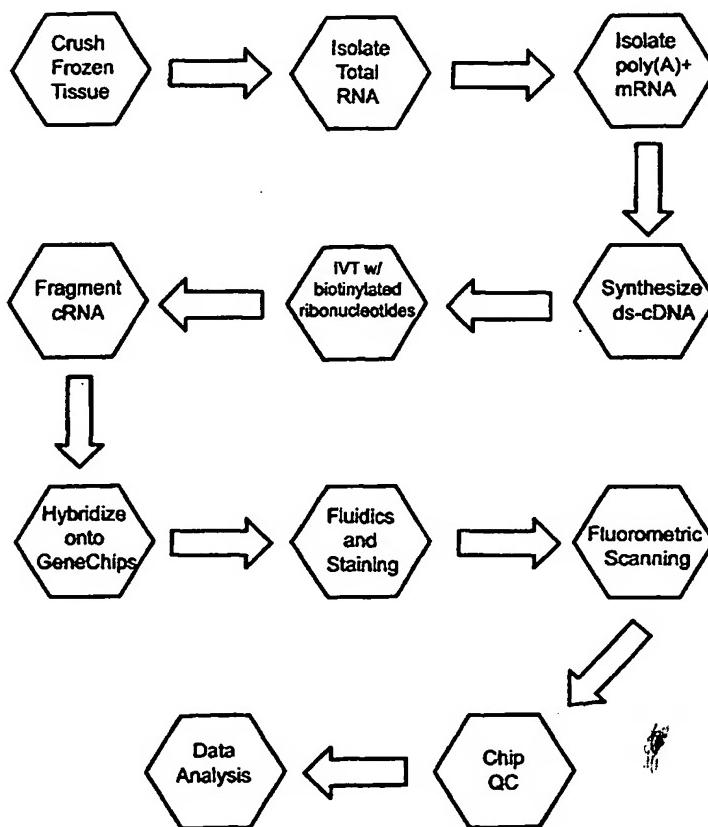
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(54) Title: GENE EXPRESSION PROFILES IN LIVER CANCER



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(57) Abstract: The present invention identifies the global changes in gene expression associated with liver cancer by examining gene expression in tissue from normal liver, metastatic malignant liver and hepatocellular carcinoma. The present invention also identifies expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.



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GENE EXPRESSION PROFILES IN LIVER CANCER**INVENTORS**

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RELATED APPLICATIONS

This application is related to U.S. Provisional Application 60/211,379, filed on June 14, 2000, and is related to U.S. Provisional Application 60/237,054, filed October 2, 2000, 5 and is related to U.S. Application 09/880,107, filed June 14, 2001, each of which is herein incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

Primary hepatocellular carcinoma (HCC) is a widespread cancer throughout the 10 world, especially prevalent where the incidence of chronic hepatitis B (HBV) and hepatitis C (HCV) viral infections are endemic (Groen, (1999) *Semin. Oncol. Nurs.* 15, 48-57; Idilman *et al.*, (1998) *J. Viral. Hepat.* 5, 110-117; Di Bisceglie *et al.*, (1998) *Hepatol.* 28, 1161-1165; Johnson, (1997) *Hepatogastroenterology* 44, 307-312; Sheu, (1997) *J. Gastroenterol. Hepatol.* 12, S309-313). Hepatocellular carcinomas are very malignant 15 tumors that generally offer a poor prognosis, dependent on the size of the tumor, the effect on normal liver functions, and the involvement of metastases. They are best treated by surgical resection, when the tumors are diagnosed at a stage where this is a viable possibility, but the recurrence rate for these cancers remains high (Johnson, (1997) *Hepatogastroenterology* 44, 307-312; Schafer & Sorrell, (1999) *Lancet* 353, 1253-1257; 20 Groen, (1999) *Semin. Oncol. Nurs.* 15, 48-57; Sitzman, (1995) *World. J. Surg.* 19, 790-794; DiCarlo, (1995) *Hepato-Gastroenterol.* 42, 222-259; Tanaka *et al.*, (1996) *Hepato-Gastroenterol.* 43, 1172-1181; El-Assal *et al.*, (1997) *Surgery* 122, 571-577).

Numerous risk factors for the development of HCC have been identified: cirrhosis, 25 HBV or HCV infection, being male, alcohol-related liver disease, exposure to aflatoxins, vinyl chloride and radioactive thorium dioxide, cigarette smoking, ingestion of inorganic arsenic, the use of oral contraceptives and anabolic steroids, iron accumulation, and various inherited metabolic disorders (hemochromatosis, glycogen storage disease, porphyria,

tyrosinemia, α -1-antitrypsin deficiency) (Di Bisceglie *et al.*, (1998) Hepatol. 28, 1161-1165; Chen *et al.*, (1997) J. Gastroenterol. Hepatol. 12, S294-308; Schafer & Sorrell (1999) Lancet 353, 1253-1257; Groen, (1999) Semin. Oncol. Nurs. 15, 48-57; Idilman *et al.*, (1998) J. Viral. Hepat. 5, 110-117; Johnson, (1997) Hepato-Gastroenterol. 44, 307-312).

- 5 In addition to liver tumors attributed to hepatocellular carcinoma, there are liver tumors that arise as metastases from primary tumors in other parts of the body. These tumors most often metastasize from the gastrointestinal organs, primarily the colon and rectum, but it is possible for metastatic liver cancers to occur from primary cancers throughout the body (Sitzman, (1990) Hepatic Neoplasia, in Bayless (editor) Current
10 Therapy in Gastroenterology and Liver Disease, Marcel Dekker; Groen, (1999) Semin. Oncol. Nurs. 15, 48-57). These cancers can be treated using the routine therapies such as chemotherapy, radiotherapy, surgical resection, liver transplantation, chemoembolization, cryosurgery, or a combination of therapies (Sitzman 1990, Groen 1999).

15 The characterization of genes that are differentially expressed in tumorigenesis is an important step in identifying those that are intimately involved in the details of a cell's transformation from normal to cancerous. Little is known about the molecular changes that take place in the liver during the course of tumor progression. While changes in the expression level of individual genes has been reported, for example, galectin-3 (Hsu *et al.*, (1999) Int. J. Cancer 81: 519-526; Iurisci *et al.*, (2000) Clin. Cancer Res. 6: 1389-1393;
20 Nakamura *et al.*, (1999) Int. J. Oncol. 15: 143-148) and pancreatic secretory trypsin inhibitor (PTSI, Ohmachi *et al.*, (1994) Int. J. Cancer 55: 728-734) the investigation of the global changes in gene expression which occur in liver have not been documented. The identification of genes that are expressed in tumor tissue at differing levels, but not expressed at any level in normal liver tissue will be very valuable for monitoring tumor
25 progression. The identification of genes and ESTs that are expressed in both types of tumors, *i. e.*, primary hepatocellular carcinomas as well as metastatic tumors of a different origin, and not in normal liver cells would be extremely valuable for the diagnosis of liver cancer. Thus there exists a need in the art for the identification of new genes and ESTs to serve as molecular markers to monitor the onset and development of liver cancer. These
30 and other needs are met by the present invention.

SUMMARY OF THE INVENTION

The present invention identifies the global changes in gene expression associated with liver cancer by examining gene expression in tissue from normal liver, metastatic malignant liver and hepatocellular carcinoma. The present invention also identifies expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

- 5 The invention includes methods of diagnosing the presence or absence of liver cancer in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in
- 10 Tables 3-9 is indicative of liver cancer. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5. In some preferred embodiments, the method may include detecting the expression level of one or more genes selected from a group consisting Tetraspan NET-6 protein; collagen, type V, alpha; and glypcan 3.
- 15 The invention also includes methods of detecting the progression of liver cancer and/or differentiating nonmetastatic from metastatic disease. For instance, methods of the invention include detecting the progression of liver cancer in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of liver cancer
- 20 progression. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

In some aspects, the present invention provides a method of monitoring the treatment of a patient with liver cancer, comprising administering a pharmaceutical composition to the patient and preparing a gene expression profile from a cell or tissue sample from the patient

25 and comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising liver cancer cells or to both. In some preferred embodiments, the gene profile will include the expression level of one or more genes in Tables 3-9. In other preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

In another aspect, the present invention provides a method of treating a patient with liver cancer, comprising administering to the patient a pharmaceutical composition, wherein

the composition alters the expression of at least one gene in Tables 3-9, preparing a gene expression profile from a cell or tissue sample from the patient comprising tumor cells and comparing the patient expression profile to a gene expression profile from an untreated cell population comprising liver cancer cells. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

In one aspect, the present invention provides a method of diagnosing hepatocellular carcinoma in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9, wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

In another aspect, the present invention provides a method of detecting the progression of hepatocellular carcinoma in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma progression.

15 In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

The present invention also provides materials and methods for monitoring the treatment of a patient with a hepatocellular carcinoma. The present invention provides a method of monitoring the treatment of a patient with hepatocellular carcinoma, comprising administering a pharmaceutical composition to the patient, preparing a gene expression profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising hepatocellular carcinoma cells or to both. In some preferred embodiments, the method may include detecting the level of expression of one or more genes from the genes listed in Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

In a related aspect, the present invention provides a method of treating a patient with hepatocellular carcinoma, comprising administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9, preparing a gene expression profile from a cell or tissue sample from the patient comprising hepatocellular carcinoma cells and comparing the patient expression profile to a

gene expression profile from an untreated cell population comprising hepatocellular carcinoma cells. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

The present invention provides a method of diagnosing a metastatic liver tumor in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9, wherein differential expression of the genes in Tables 3-9 is indicative of a metastatic liver tumor. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

The present invention provides a method of detecting the progression of a metastatic liver tumor in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9, wherein differential expression of the genes in Tables 3-9 is indicative of a metastatic liver tumor progression. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

In a related aspect, the present invention provides a method of monitoring the treatment of a patient with a metastatic liver tumor, comprising administering a pharmaceutical composition to the patient, preparing a gene expression profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising metastatic liver tumor cells or to both. In some preferred embodiments, the method of the present invention may include detecting the expression level of one or more genes selected from the genes listed in Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

In some preferred embodiments, the present invention provides a method of treating a patient with a metastatic liver tumor, comprising administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9, preparing a gene expression profile from a cell or tissue sample from the patient comprising metastatic liver tumor cells and comparing the patient expression profile to a gene expression profile from an untreated cell population comprising metastatic liver tumor cells. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

The invention also includes methods of differentiating metastatic liver cancer from hepatocellular carcinoma in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of metastatic liver cancer rather than hepatocellular carcinoma.

5 The invention further includes methods of screening for an agent capable of modulating the onset or progression of liver cancer, comprising the steps of exposing a cell to the agent; and detecting the expression level of two or more genes from Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of 10 the genes listed in Tables 3-5.

Any of the methods of the invention described above may include the detection of at least 2 genes from the tables. Preferred methods may detect all or nearly all of the genes in the tables. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

15 The invention further includes compositions comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 3-9 as well as solid supports comprising at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 3-9. In some preferred embodiments, one or more genes may be selected 20 from a group consisting of the genes listed in Tables 3-5.

The invention further includes computer systems comprising a database containing information identifying the expression level in liver tissue of a set of genes comprising at least two genes in Tables 3-9; and a user interface to view the information. In some preferred embodiments, one or more genes may be selected from a group consisting of the 25 genes listed in Tables 3-5. The database may further include sequence information for the genes, information identifying the expression level for the set of genes in normal liver tissue and malignant tissue (metastatic and nonmetastatic) and may contain links to external databases such as GenBank.

Lastly, the invention includes methods of using the databases, such as methods of 30 using the disclosed computer systems to present information identifying the expression level in a tissue or cell of at least one gene in Tables 3-9, comprising the step of comparing the expression level of at least one gene in Tables 3-9 in the tissue or cell to the level of

expression of the gene in the database. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

BRIEF DESCRIPTION OF THE DRAWINGS

- 5 Figure 1 is a flow chart showing a schematic representation of the experimental protocol.

Figures 2A-2C are graphs of the number of genes present in all samples as a function of the number of samples for the second sample set.

10 DETAILED DESCRIPTION

Many biological functions are accomplished by altering the expression of various genes through transcriptional (*e.g.*, through control of initiation, provision of RNA precursors, RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death, are often characterized by the variations in the expression levels of groups of genes.

Changes in gene expression also are associated with pathogenesis. For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over expression of oncogene/protooncogenes could lead to tumorigenesis or hyperplastic growth of cells (Marshall, (1991) Cell, 64, 313-326; Weinberg, (1991) Science, 254, 1138-1146).
20 Thus, changes in the expression levels of particular genes (*e.g.*, oncogenes or tumor suppressors) serve as signposts for the presence and progression of various diseases.

Monitoring changes in gene expression may also provide certain advantages during drug screening development. Often drugs are screened and prescreened for the ability to interact with a major target without regard to other effects the drugs have on cells. Often
25 such other effects cause toxicity in the whole animal, which prevent the development and use of the potential drug.

The present inventors have examined tissue samples from normal liver, metastatic malignant liver and hepatocellular carcinoma to identify the global changes in gene expression associated with liver cancer. The protocol used is schematically represented in
30 Figure 1. These global changes in gene expression, also referred to as expression profiles, provide useful markers for diagnostic uses as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Definitions

In the description that follows, numerous terms and phrases known to those skilled in the art are used. In the interests of clarity and consistency of interpretation, the 5 definitions of certain terms and phrases are provided.

The present invention provides compositions and methods to detect the level of expression of genes that may be differentially expressed dependent upon the state of the cell, *i.e.*, normal versus cancerous. As used herein, the phrase "detecting the level of expression" includes methods that quantitate expression levels as well as methods that determine 10 whether a gene of interest is expressed at all. Thus, an assay which provides a yes or no result without necessarily providing quantification of an amount of expression is an assay that requires "detecting the level of expression" as that phrase is used herein.

As used herein, oligonucleotide sequences that are complementary to one or more of the genes described herein, refers to oligonucleotides that are capable of hybridizing under 15 stringent conditions to at least part of the nucleotide sequence of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

"Bind(s) substantially" refers to complementary hybridization between a probe 20 nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target 25 nucleic acids and components of the oligonucleotide array (*e.g.*, the oligonucleotide probes, control probes, the array substrate, etc.). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the 30 average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that

where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in 5 the sample (e.g., probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all.

The phrase "hybridizing specifically to" refers to the binding, duplexing or 10 hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA.

The term "mismatch control" or "mismatch probe" refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence. 15 For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases.

While the mismatch(s) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization 20 of the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most likely to destabilize the duplex with the target sequence under the test hybridization conditions.

The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly 25 complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe."

As used herein a "probe" is defined as a nucleic acid, capable of binding to a target 30 nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, U, C or T) or modified bases (7-

deazaguanosine, inosine, etc.). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

- 5 The term "stringent conditions" refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are
10 selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.

- Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotide). Stringent
15 conditions may also be achieved with the addition of destabilizing agents such as formamide.

- The "percentage of sequence identity" or "sequence identity" is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may 20 optionally comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical monomer unit (e.g., nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched
25 positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

- Homology or identity may be determined by BLAST (Basic Local Alignment
30 Search Tool) analysis using the algorithm employed by the programs **blastp**, **blastn**, **blastx**, **tblastn** and **tblastx** (Karin *et al.*, (1990) Proc. Natl. Acad. Sci. USA 87, 2264-2268 and Altschul, (1993) J. Mol. Evol. 36, 290-300, fully incorporated by reference) which are

tailored for sequence similarity searching. The approach used by the BLAST program is to first consider similar segments between a query sequence and a database sequence, then to evaluate the statistical significance of all matches that are identified and finally to summarize only those matches which satisfy a preselected threshold of significance. For a 5 discussion of basic issues in similarity searching of sequence databases, see Altschul *et al.*, (1994) *Nature Genet.* 6, 119-129) which is fully incorporated by reference. The search parameters for histogram, descriptions, alignments, expect (*i.e.*, the statistical significance threshold for reporting matches against database sequences), cutoff, matrix and filter are at the default settings. The default scoring matrix used by blastp, blastx, tblastn, and tblastx 10 is the BLOSUM62 matrix (Henikoff *et al.*, (1992) *Proc. Natl. Acad. Sci. USA* 89, 10915-10919, fully incorporated by reference). Four blastn parameters were adjusted as follows: Q=10 (gap creation penalty); R=10 (gap extension penalty); wink=1 (generates word hits at every winkth position along the query); and gapw=16 (sets the window width within which gapped alignments are generated). The equivalent Blastp parameter settings were Q=9; 15 R=2; wink=1; and gapw=32. A Bestfit comparison between sequences, available in the GCG package version 10.0, uses DNA parameters GAP=50 (gap creation penalty) and LEN=3 (gap extension penalty) and the equivalent settings in protein comparisons are GAP=8 and LEN=2.

20 *Uses for the Liver Cancer Markers as Diagnostics*

As described herein, the genes and gene expression information provided in Tables 3-9 may be used as diagnostic markers for the prediction or identification of the malignant state of the liver tissue. For instance, a liver tissue sample or other sample from a patient may be assayed by any of the methods described herein or by any other method known to 25 those skilled in the art, and the expression levels from a gene or genes from the Tables, in particular the genes in Tables 3-5, may be compared to the expression levels found in normal liver tissue, tissue from metastatic liver cancer or hepatocellular carcinoma tissue. Expression profiles generated from the tissue or other sample that substantially resemble an expression profile from normal or diseased liver tissue may be used, for instance, to aid in 30 disease diagnosis. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described above.

Use of the Liver Cancer Markers for Monitoring Disease Progression

As described above, the genes and gene expression information provided in Tables 3-9 may also be used as markers for the monitoring of disease progression, for instance, the development of liver cancer. For instance, a liver tissue sample or other sample from a patient may be assayed by any of the methods described above, and the expression levels in the sample from a gene or genes from 3-9 may be compared to the expression levels found in normal liver tissue, tissue from metastatic liver cancer or hepatocellular carcinoma tissue. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described above.

Use of the Liver Cancer Markers for Drug Screening

According to the present invention, the genes identified in Tables 3-9 may be used as markers to evaluate the effects of a candidate drug or agent on a cell, particularly a cell undergoing malignant transformation, for instance, a liver cancer cell or tissue sample. A candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or markers (drug targets) or to down-regulate or counteract the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of drugs' effects by looking at the number of markers affected by different drugs and comparing them. More specific drugs will affect fewer transcriptional targets. Similar sets of markers identified for two drugs indicates a similarity of effects.

Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agents action. Agents can be rationally

selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

- The agents of the present invention can be, as examples, peptides, small molecules, 5 vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNA encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" as used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally 10 similar to the parent peptide (see Grant, (1995) in Molecular Biology and Biotechnology Meyers (editor) VCH Publishers). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

Assay Formats

- 15 The genes identified as being differentially expressed in liver cancer may be used in a variety of nucleic acid detection assays to detect or quantitate the expression level of a gene or multiple genes in a given sample. Any hybridization assay format may be used, including solution-based and solid support-based assay formats, for example, traditional Northern blotting. Other suitable assay formats that may be used for detecting gene 20 expression levels include, but are not limited to, nuclease protection, RT-PCR and differential display methods. These methods are useful for some embodiments of the invention; however, methods and assays of the invention are most efficiently designed with array or chip hybridization-based methods for detecting the expression of a large number of genes. Assays and methods of the invention may utilize available formats to simultaneously 25 screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 1,000,000 or more different nucleic acid hybridizations.

- Assays to monitor the expression of a marker or markers as defined in Tables 3-9 may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression 30 of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

In one assay format, gene chips containing probes to at least two genes from Tables

3-9 may be used to directly monitor or detect changes in gene expression in the treated or exposed cell as described in more detail above. In another format, cell lines that contain reporter gene fusions between the open reading frame and/or the 3' or 5' regulatory regions of a gene in Tables 3-9 and any assayable fusion partner may be prepared. Numerous
5 assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.*, (1990) *Anal. Biochem.* 188, 245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents
10 which modulate the expression of the nucleic acid.

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of one or more genes identified in Tables 3-9. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under
15 appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.*, (1989) *Molecular Cloning - A Laboratory Manual*, Cold Spring Harbor Laboratory Press).

In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically. Cell and/or cell lines so identified would be
20 expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Such cell lines may be, but are not required to be, derived from liver tissue. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector)
25 construct comprising an operable non-translated 5'-promoter containing end of the structural gene encoding the instant gene products fused to one or more antigenic fragments, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further
30 comprise an immunologically distinct tag. Such a process is well known in the art (see Sambrook *et al.*, (1989) *Molecular Cloning - A Laboratory Manual*, Cold Spring Harbor Laboratory Press).

- Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt
- 5 solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells will be disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed
- 10 by immunological assay (e.g., ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agent-contacted" sample will be compared with a control sample where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control will be used to distinguish the effectiveness of the agent.
- 15 Another embodiment of the present invention provides methods for identifying agents that modulate the levels, concentration or at least one activity of a protein(s) encoded by the genes in Tables 3-9. Such methods or assays may utilize any means of monitoring or detecting the desired activity.
- In one format, the relative amounts of a protein of the invention between a cell
- 20 population that has been exposed to the agent to be tested compared to an un-exposed control cell population may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell
- 25 line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may be cloned or not and the genes may be amplified or not. The cloning itself does not appear to bias the representation

30 of genes within a population. However, it may be preferable to use polyA+ RNA as a source, as it can be used with less processing steps.

The sequences of the expression marker genes are in the public databases. Tables 3-9 provide the Affymetrix gene ID and GenBank accession number for each marker identified. The nucleotide sequence for each marker has been provided in electronic format with this application and these sequences are incorporated herein by reference as are
5 equivalent and related sequences present in the public databases.

Probes based on the sequences of the genes described herein may be prepared by any commonly available method. Oligonucleotide probes for assaying the tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least 10,
10 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases longer probes of at least 30, 40, or 50 nucleotides will be desirable.

Probe design

One of skill in the art will appreciate that an enormous number of array designs are
15 suitable for the practice of this invention. The high density array will typically include a number of probes that specifically hybridize to the sequences of interest. See WO 99/32660 for methods of producing probes for a given gene or genes. In addition, in a preferred embodiment, the array will include one or more control probes.

High density array chips of the invention include "test probes." Test probes may be
20 oligonucleotides that range from about 5 to about 500 or about 5 to about 50 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 40 nucleotides in length. In other particularly preferred embodiments the probes are about 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences. DNA sequences are isolated or cloned from
25 natural sources or amplified from natural sources using natural nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.

In addition to test probes that bind the target nucleic acid(s) of interest, the high
30 density array can contain a number of control probes. The control probes fall into three categories referred to herein as (1) normalization controls; (2) expression level controls; and (3) mismatch controls.

Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (e.g., fluorescence intensity) read from all other probes in the array are divided by the signal (e.g., fluorescence intensity) from the control probes thereby normalizing the measurements.

Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base composition of the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they are selected such that they hybridize well (*i.e.*, no secondary structure) and do not match any target-specific probes.

Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typical expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to the β -actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (e.g., stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a

probe is a twenty-mer, a corresponding mismatch probe will have the identical sequence except for a single base mismatch (*e.g.*, substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

- Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is directed. Mismatch probes also indicate whether a hybridization is specific or not. For example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation. The difference in intensity between the perfect match and the mismatch probe ($I_{(PM)} - I_{(MM)}$) provides a good measure of the concentration of the hybridized material.

Nucleic Acid Samples

- As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process. Methods of isolating total mRNA are also well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I Theory and Nucleic Acid Preparation, Tijssen, (1993) 20 (editor) Elsevier Press. Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and an RNA transcribed from the amplified DNA. One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates can be used.
- 25 Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised *in vitro*, such as cell lines and tissue culture cells. Frequently the sample will be a "clinical sample" which is a sample derived from a patient. Typical clinical samples include, but are not limited to, sputum, blood, blood-cells (*e.g.*, white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, 30 or cells therefrom.

Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

Solid Supports

Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, silicon or glass based chips, etc.

- 5 Such wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755). Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined
- 10 location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, about 2, 10, 100, 1000 to 10,000; 100,000 or 400,000 of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of a square centimeter.
- 15 Oligonucleotide probe arrays for expression monitoring can be made and used according to any techniques known in the art (see for example, Lockhart *et al.*, (1996) Nat. Biotechnol. 14, 1675-1680; McGall *et al.*, (1996) Proc. Nat. Acad. Sci. USA 93, 13555-13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described herein. Such arrays
- 20 may also contain oligonucleotides that are complementary or hybridize to at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70, 100 or more the genes described herein.

Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a solid substrate by a variety of methods, including, but not limited to, light-directed chemical coupling, and mechanically directed coupling (see Pirrung *et al.*, (1992) U.S. Patent No. 5,143, 854; Fodor *et al.*, (1998) U.S. Patent No. 5,800,992; Chee *et al.*, (1998) 5,837,832.

- In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane reagent containing a functional group, e.g., a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithographic mask is used selectively to expose functional groups which are then ready to react with incoming 5'
- 30

- photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been
- 5 synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.
- In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in Fodor *et al.*, (1993). WO
10 93/09668. High density nucleic acid arrays can also be fabricated by depositing premade or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

15

Hybridization

- Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing (see Lockhart *et al.*, (1999) WO 99/32660).
- 20 The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids.
- Under low stringency conditions (*e.g.*, low temperature and/or high salt) hybrid
25 duplexes (*e.g.*, DNA-DNA, RNA-RNA or RNA-DNA) will form even where the annealed sequences are not perfectly complementary.
- Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (*e.g.*, higher temperature or lower salt) successful hybridization requires fewer mismatches. One of skill in the art will appreciate that hybridization conditions may
30 be selected to provide any degree of stringency. In a preferred embodiment, hybridization is performed at low stringency, in this case in 6× SSPE-T at 37°C (0.005% Triton x-100) to ensure hybridization and then subsequent washes are performed at higher stringency (*e.g.*,

1× SSPE-T at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (e.g., down to as low as 0.25× SSPE-T at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be 5 evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (e.g., expression level control, normalization control, mismatch controls, etc.).

In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest 10 stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides 15 adequate signal for the particular oligonucleotide probes of interest.

Signal Detection

The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of 20 means well known to those of skill in the art (see Lockhart *et al.*, (1999) WO 99/32660).

Databases

The present invention includes relational databases containing sequence information, for instance for the genes of Tables 3-9, as well as gene expression information in various 25 liver tissue samples. Databases may also contain information associated with a given sequence or tissue sample such as descriptive information about the gene associated with the sequence information, or descriptive information concerning the clinical status of the tissue sample, or the patient from which the sample was derived. The database may be designed to include different parts, for instance a sequences database and a gene expression database. 30 Methods for the configuration and construction of such databases are widely available, for instance, see Akerblom *et al.*, (1999) U.S. Patent 5,953,727, which is herein incorporated by reference in its entirety.

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The databases of the invention may be linked to an outside or external database. In a preferred embodiment, as described in Tables 3-9, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI).

- 5 Any appropriate computer platform may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such as those available from Silicon Graphics. Client-server environments, database servers and networks
10 are also widely available and appropriate platforms for the databases of the invention.

The databases of the invention may be used to produce, among other things, electronic Northerns to allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell.

- 15 The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising at least one gene in Tables 3-9 comprising the step of comparing the expression level of at least one gene in Tables 3-9 in the tissue to the level of expression of the gene in the database. Such methods may be used to predict the physiological state of a given tissue by comparing the level of
20 expression of a gene or genes in Tables 3-9 from a sample to the expression levels found in tissue from normal liver, malignant liver or hepatocellular carcinoma. Such methods may also be used in the drug or agent screening assays as described below.

- Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the
25 compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

EXAMPLES

- 30 Example 1: Tissue Sample Acquisition and Preparation

Figure 1 outlines the experimental protocol used. Liver tissue samples were excised and snap frozen in liquid nitrogen. The clinical data for each of the samples included in this

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study are outlined in Table 1. The sample set was composed of eight samples of normal liver tissue (N1-N8), five samples of metastatic adenocarcinoma arising from rectum (designated M1 and M3) and colon (M2, M4 and M5) tissues and six samples of primary hepatocellular carcinomas. Samples were named according to type of tissue:

- 5 HCC=hepatocellular carcinoma, M=metastatic, N=normal. Table 1 includes the TNM classification (the American Joint Committee on Cancer's system of classifying cancers) of the tissues used as samples where T refers to the extent of the primary tumor, N refers to the absence or presence and extent of regional lymph node metastasis, and M refers to the absence or presence of distant metastasis. Numbers following T, N, and M refer to the size
10 of the primary tumor and the amount of vascular invasion, where 0=no evidence of tumor, lymph node involvement or metastasis, 4=multiple tumors involved, and x=cannot be assessed. Histopathologic grade (Table 1) is a qualitative assessment of differentiation of a tumor, where G1=most differentiated and G4=undifferentiated. Clinical stage (Table 1) characterizes the anatomic extent of disease in the patient from whom the sample was taken,
15 where I and II are early stages, III and IV are late stages.

With minor modifications, the sample preparation protocol followed the Affymetrix GeneChip Expression Analysis Manual. Frozen tissue was first ground to powder using the Spex Certiprep 6800 Freezer Mill. Total RNA was then extracted using Trizol (Life Technologies). The total RNA yield for each sample (average tissue weight of 300 mg) was
20 200-500 µg. Next, mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen). Since the mRNA was eluted in a final volume of 400 µl, an ethanol precipitation step was required to bring the concentration to 1 µg/µl. Using 1-5 µg of mRNA, double stranded cDNA was created using the SuperScript Choice system (Gibco-BRL). First strand cDNA synthesis was primed with a T7-(dT₂₄) oligonucleotide. The cDNA was then phenol-chloroform
25 extracted and ethanol precipitated to a final concentration of 1 µg/µl.

From 2 µg of cDNA, cRNA was synthesized according to standard procedures. To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. After a 37°C incubation for six hours, the labeled cRNA was cleaned up according to the Rneasy Mini kit protocol (Qiagen). The cRNA was then fragmented (5×
30 fragmentation buffer: 200 mM Tris-Acetate (pH 8.1), 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C.

55 µg of fragmented cRNA was hybridized on the human Hu35k set and the

HuGeneFL array for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between.

- 5 Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Following hybridization and scanning, the microarray images were analyzed for quality control, looking for major chip defects or abnormalities in hybridization signal. After all chips passed QC, the data was analyzed using Affymetrix GeneChip software (v3.0), and Experimental Data Mining Tool (EDMT) software (v1.0).

10

Example 2: Gene Expression Analysis

- All samples were prepared as described and hybridized onto the Affymetrix HuGeneFL array and the Human Hu35k set of arrays. Each chip contains 16-20 oligonucleotide probe pairs per gene or cDNA clone. These probe pairs include perfectly 15 matched sets and mismatched sets, both of which are necessary for the calculation of the average difference. The average difference is a measure of the intensity difference for each probe pair, calculated by subtracting the intensity of the mismatch from the intensity of the perfect match. This takes into consideration variability in hybridization among probe pairs and other hybridization artifacts that could affect the fluorescence intensities. Using the 20 average difference value that has been calculated, the GeneChip software then makes an absolute call for each gene or EST.

- The absolute call of present, absent or marginal is used to generate a Gene Signature, a tool used to identify those genes that are commonly present or commonly absent in a given sample set, according to the absolute call. For each set of samples, a median average 25 difference was figured using the average differences of each individual sample within the set. The median average difference must be greater than 150 to assure that the expression level is well above the background noise of the hybridization. For the purposes of this study, only the genes and ESTs with a median average difference greater than 150 have been further studied in detail.

- 30 The Gene Signature for one set of samples is compared to the Gene Signature of another set of samples to determine the Gene Signature Differential. This comparison identifies the genes that are consistently present in one set of samples and consistently

absent in the second set of samples.

The Gene Signature Curve is a graphic view of the number of genes consistently present in a given set of samples as the sample size increases, taking into account the genes commonly expressed among a particular set of samples, and discounting those genes whose expression is variable among those samples. The curve is also indicative of the number of samples necessary to generate an accurate Gene Signature. As the sample number increases, the number of genes common to the sample set decreases. The curve is generated using the positive Gene Signatures of the samples in question, determined by adding one sample at a time to the Gene Signature, beginning with the sample with the smallest number of present genes and adding samples in ascending order. The curve displays the sample size required for the most consistency and the least amount of expression variability from sample to sample. The point where this curve begins to level off represents the minimum number of samples required for the Gene Signature. Graphed on the x-axis is the number of samples in the set, and on the y-axis is the number of genes in the positive Gene Signature.

15

Example 3: Gene Expression Analysis of Normal Liver Tissue

The gene expression patterns and Gene Signature were individually determined for each sample set: eight samples with normal liver pathology, six samples whose pathology indicated the primary malignancy to be hepatocellular carcinoma, and five samples whose primary colorectal adenocarcinoma had metastasized to the liver. The Gene Signatures obtained for the normal sample set is shown in Figure 2A, the metastatic liver cancer set in Figure 2B and the hepatocellular carcinoma set in Figure 2C.

The Gene Signature considers the present and absent genes alone, and does not take into consideration those that have been called marginal. Table 2 shows the numbers of 25 present genes, called the positive Gene Signature, and the number of absent genes, called the negative Gene Signature, for each of the three sets of samples.

The Gene Signature is the set of genes that are commonly present or commonly absent in N-1 samples of a given sample set. The positive Gene Signature for the normal liver tissues contains 6,213 genes and ESTs. This same set of normal samples did not show 30 any detectable level of expression of 24,900 genes. Many of the genes and ESTs in this positive Gene Signature are housekeeping genes or structural genes that are not only expressed in the liver, but are ubiquitously expressed in tissues throughout the body. Within

this positive Gene Signature are also those genes whose expression is specifically restricted to normal liver tissue and those genes required for the liver to function at its normal capacities. It is the group of genes unique to the liver whose expression levels are most likely to change during tumorigenesis. Whether up-regulated or down-regulated or turned 5 completely on or turned completely off, the changes in expression of these vital genes very likely contributes to the drastic changes in liver function caused by the transformation of normal liver cells into cancerous cells.

Example 4: Gene Expression Analysis of Malignant Liver Tissue

10 There are 8,479 genes and ESTs in the positive Gene Signature for the HCC tumors, and a total of 23,233 genes and ESTs are included in the negative Gene Signature of the HCC samples. This negative Gene Signature includes all the genes that have been completely turned off during tumorigenesis, as well as those genes that are not usually expressed in liver tissue. These results include a number of genes and ESTs that are not 15 regularly expressed in liver tissues, but through the process of tumor production, their expression patterns have been dramatically altered from no detectable level of expression to some significant level of expression in comparison with the normal liver.

The colorectal metastases in the liver commonly express 5,102 genes and ESTs, and do not show expression of 30,455 additional genes and ESTs. As with the negative Gene 20 Signature for the HCC sample set, the genes included in this data set are generally not expressed in liver tissue, whether tumor or normal tissue. The 5,102 in the sample set of metastatic tumors also identify those genes with expression levels that have been changed from off to on as a result of tumor formation.

25 **Example 5: Analysis of Gene Expression Profiles**

A differential comparison of the genes and ESTs expressed in the normals and the two different types of liver tumors identifies a subset of the genes included in the positive Gene Signatures that are uniquely expressed in each sample set. This Gene Signature Differential highlights genes whose expression profiles have most dramatically changed in 30 the transformation from normal to diseased liver cells. The parameters for these analyses were set to accommodate variation in expression of one of eight normal samples and one of the six HCC samples or one of the 5 metastatic tumor samples, such that the genes

categorized as unique to normal were called present by the software in seven of eight (87%) normal liver samples and were also called absent in five of six HCC (83%) or four of five (80%) metastatic liver tumor. Conversely, the genes categorized as unique to each set of tumors as compared to the normal livers were called present in five of six HCC (83%) or 5 four of five (80%) metastatic tumor samples and absent in seven of eight normal livers (87%).

The Gene Signature Differential comparing the normal livers to those with metastatic tumors identified a total of 903 sequences expressed only in normal liver tissue. The number of genes or ESTs that meet the median average difference minimum of 150 is 10 449, of which 289 are genes and the number of ESTs is 160. The remaining ESTs and genes may be indistinguishable from the background noise of the hybridization. The same comparison of normals versus metastatic tumors demonstrates that in the metastatic tumor samples there are 296 uniquely expressed sequences. Those that meet the median average difference minimum requirement are 83 genes and 72 ESTs. Those genes and ESTs 15 expressed in metastatic and not in normal liver tissue are shown in Table 9A and those present in normal liver tissue and not metastatic tissue Table 9B. Numerous genes with differing expression levels in metastatic liver tumor tissue compared to normal tissue were identified. The fifteen genes whose expression level was most different in metastatic as compared to normal tissue are shown in Table 4. Those with the most increased expression 20 are in Table 4A and those with the most decreased expression are in Table 4B. Expression levels were determined by comparing the mean expression values of individual genes in tumor and normal liver samples. Fold change was calculated as a ratio with a p value given as a measure of statistical significance. Fold change is considered significant for a given gene or EST when it is greater than 3.0 with a p value <0.05. Only the characterized genes 25 have been listed; the ESTs with similar fold changes are not presented here. Asterisk (*) in Table 4 denotes those genes that were also identified in the Gene Signature differential between metastatic liver carcinoma and normal liver tissue. A complete listing of all the genes and ESTs with at least a three-fold change in expression is shown in Table 6. Table 6A contains those genes and ESTs whose expression level increased in metastatic tissue 30 relative to normal tissue and Table 6B contains those genes and ESTs whose expression level decreased.

The Gene Signature Differential between the normal liver samples and the HCC

samples identifies a total of 47 unique expressers in the normals, 23 with an median average difference of 150 ,13 of which are named gene and 10 of which are ESTs. When comparing the expression of the HCC samples with the normal livers, there are 243 genes and ESTs only expressed in the HCC samples.

5 Those genes and ESTs expressed in HCC and not in normal liver tissue are shown in Table 8A and those present in normal liver tissue and not HCC tissue in Table 8B. Numerous genes with differing expression levels in HCC compared to normal tissue were identified. The fifteen genes whose expression level was most different in HCC as compared to normal tissue are shown in Table 3. Those with the most increased expression
10 are in Table 3A and those with the most decreased expression are in Table 3B. Expression levels were determined by comparing the mean expression values of individual genes in tumor and normal liver samples. Fold change was calculated as a ratio with a p value given as a measure of statistical significance. Fold change is considered significant for a given gene or EST when it is greater than 3.0 with a p value <0.05. Only the characterized genes
15 have been listed; the ESTs with similar fold changes are not presented here. Asterisk (*) denotes those genes that were also identified in the Gene Signature differential between hepatocellular carcinoma and normal liver tissue. A complete listing of all the genes and ESTs with at least a three-fold change in expression is shown in Table 7. Table 7A contains those genes and ESTs whose expression level increased in hepatocellular carcinoma tissue
20 relative to normal tissue and Table 7B contains those genes and ESTs whose expression level decreased.

Analysis of sample set identified 24 ESTs and 42 genes that are expressed in both metastatic liver tumors and hepatocellular carcinomas, but not in normal liver tissues. The fifteen genes with the most increase in expression level in both types of cancer are shown in
25 Table 5. Expression levels were determined by comparing the mean expression values of individual genes in tumor and normal liver samples. The mean expression value for HCC and metastatic carcinomas was greater than 250, and included only those genes that showed a fold change greater than 3 with significant p values for both sets of tumors. No detectable level of expression was found in the normal liver tissues for these genes. Only the
30 characterized genes have been listed; the ESTs with similar fold changes that are unique to the tumors are not presented here.

Differential gene expression patterns between normal liver samples and

hepatocellular carcinomas and between normal livers and metastatic liver tumors were examined. Genes uniquely expressed by each of the groups individually were identified, as well as those genes that are commonly expressed among liver tumors, whether primary hepatocellular carcinomas or metastatic liver tumors.

5

Example 6: Association of Liver Cancer with Specific Gene Expression

The present inventors have closely examined a number of the tumor-expressing genes to determine if their expression patterns correlate with previous reports published in the literature, and to define a logical relationship between the gene and

10 hepatocarcinogenesis. A number of genes that have previously been associated with either liver cancer or other types of cancers were identified, as well as numerous genes that have not been linked to cancers in any previous studies.

842 genes and ESTs that are up-regulated in hepatocellular carcinomas were identified when compared with normal liver tissue. One such gene is PTTG1, pituitary 15 tumor-transforming gene 1, or securin, an oncogene that inhibits sister chromatid separation during anaphase. Normal tissues show little or no PTTG1 expression, but high levels of expression have been associated with various tumors, including liver tumors, and carcinoma cell lines. Overexpression in NIH3T3 cells resulted in transformation, and these cells caused the formation of tumors when injected into mice. The mechanism by which this 20 tumorigenic activity takes place is postulated to be through the missegregation of sister chromatids, resulting in aneuploidy and, therefore, genetic instability. Our data further support this overexpression of PTTG1 in hepatocellular carcinoma, with a fold change of 10.7 ($P=0.00052$), and no detectable level of expression in normal tissues, as identified by the differential comparison of the consensus patterns of gene expression of these two sample 25 sets.

Galectin 3, LGALS3, one of a family of beta-galactoside-binding animal lectins, is significantly overexpressed both in primary hepatocellular carcinoma and metastatic liver carcinomas with fold changes of 6.8 ($P=0.00103$) and 27.1 ($P=0.00001$), respectively.

Expression of LGALS3 has been associated with tumor growth, progression, and metastasis, 30 as well as cell-cell and cell-matrix interactions and inflammatory processes. Although expression studies by Hsu *et al.* revealed no detectable level of galectin-3 in normal liver cells, samples from patients with hepatocellular carcinoma revealed considerable levels of

LGALS3 expression. The abnormal expression of this lectin may be an early event in the process of transformation of normal cells to tumor cells, or it may impart an increased capacity for these tumor cells to survive and proliferate. Consistent with the reports by Iurisci *et al* and Nakamura *et al*, an increased expression level was found in both types of tumor, but higher concentrations of galectin-3 were observed in liver metastases from colorectal tumors than in the primary HCC tumors.

Another gene that is overexpressed in both hepatocellular carcinoma and metastatic colorectal adenocarcinomas with fold changes of 12.2 ($P=0.00169$) and 58.0 ($P=0.00063$), respectively, is solute carrier family 2, member 3, or glucose transporter 3 (GLUT3). It is one of a family of transmembrane proteins that function as facilitative glucose transporters, which has a unique specificity for brain and neuronal tissues. Glucose uptake and metabolism are known to be increased in carcinoma cells compared to normal cells. Glucose transporter expression may be elevated in response to the increase in glucose utilization seen in actively proliferating cells, like those of tumors. Conversely, the high levels of glucose transporter expression may be responsible for the enhanced influx of glucose into the tumor cells. Various reports have indicated increased expression of one or more of the family of glucose transporters in malignancies, including those of the brain, esophagus, colon, pancreas, liver, breast, lung, bladder, ovary, testis, skin, head and neck, kidney, and gastric tumors. Kurata *et al.* (Jpn J Cancer Res 1999 Nov;90(11):1238-43) specifically report that metastatic liver carcinomas have even higher levels of GLUT3 expression than primary tumors. Consistent with previous studies, the current data confirm the significant overexpression of GLUT3 both in primary liver cancer, hepatocellular carcinoma, and in tumors that have metastasized from the colon and rectum.

One of the significantly underexpressed genes identified by comparing the expression profiles of hepatocellular carcinomas and metastatic liver tumors with that of normal liver tissue is metallothionein 1L. The expression level in HCC is 26.9 fold lower than that of normal ($P=0.00999$), and in metastatic colorectal adenocarcinomas it is down-regulated 66.5 fold ($P=0.00415$). Metallothioneins are heavy metal binding proteins that are involved in detoxification of metals, zinc and copper metabolism cellular adaptation mechanisms, and may be involved in regulating apoptosis. Colorectal adenocarcinoma that has metastasized to the liver has been specifically reported to express less metallothionein than normal liver tissue. Comparison of the consensus patterns of gene expression between

metastatic liver samples and normal liver samples show no significant level of MT1L expression in the tumors. Furthermore, additional work has determined that human hepatocellular carcinomas contain much lower levels of metallothioneins than normal liver tissue, and that this decrease correlates with the degree of differentiation and concentrations of copper and zinc in the cells. By comparing the expression profiles of hepatocellular carcinoma and normal liver tissue, this significant reduction in MT1L expression in HCC was confirmed.

- A number of enzymes belonging to the family of cytochrome P450s are drastically underexpressed in the two sets of liver tumors in comparison with the normal liver tissue.
- 10 For example, expression of CYP2A6 is decreased in HCC with a fold change of 14.2 ($P=0.0307$), and in metastatic tumors with a fold change of 69.9 ($P=0$). CYP8B1 is down-regulated 19.3 fold ($P=0.00807$) in HCC and 65.1 fold ($P=0.0039$) in liver metastases. In addition to these commonly down-regulated cytochrome P450s, in HCC samples CYP2B is underexpressed 17.9 fold ($P=0.01469$), and in the metastatic liver tumors CYP2C9 and
- 15 CYP2A7 are underexpressed 84.7 fold ($P=0.00327$) and 72.0 fold ($P=0$), respectively. Several of these genes are also identified by the differential comparison between expression profiles of tumor and normal, confirming the significant decrease in expression in tumor tissues. Many of these P450 enzymes are critical players in the metabolism of carcinogens, drugs, and other chemical compounds, that are expressed in normal liver.
- 20 In addition to genes that are underexpressed in metastatic adenocarcinomas in the liver, more than 1000 genes and ESTs that are overexpressed specifically in these tumors were identified. Two of the most highly up-regulated are claudin 4, also known as clostridium perfringens enterotoxin receptor 1 (fold change 84.4, $P=0$) and occludin (fold change 43.1, $P=0$). Both of these genes are tight junction proteins, responsible for the
- 25 formation and maintenance of continuous seals around epithelial cells to form a physical barrier that blocks the free passage of water and solutes through the paracellular space. More specifically, claudin-4 is one member of a family of transmembrane proteins that comprise tight junction strands, and occludin is a cell adhesion molecule (Morita *et al.*, (1999) Proc. Natl. Acad. Sci. U.S.A. 96: 511-516). Claudins likely function as paracellular channels, regulating the flow of ions and solutes into and out of the paracellular space
- 30 (Simon *et al.*, (1999) Science 235: 103-106; Wong & Goodenough (1999) Science 285: 62; Anderson & Van Itallie (1999) Curr. Biol. 9: R922-924). Tight junction proteins also

contribute to the regulation of the cellular processes of cell growth and differentiation (Matter & Balda (1999) *Int. Rev. Cytol.* 186: 117-146). Permeability of tight junctions has been associated with tumor formation, where a breakdown in the barrier function of tight junctions allows an increase in the cellular permeability. This breakdown then opens the 5 tight junction barrier, permitting invasion by tumor cells (Zak *et al.*, (2000) *Pflugers Arch.* 440: 179-183; Mullin (1997) *J. Exp. Zool.* 279: 484-489). It has been reported that tight junctions of colon tumors leak more than do the tight junctions of normal colon (Soler *et al.*, (1999) *Carcinogenesis* 20: 1425-1431). A complete loss of tight junction function and a 10 loss of cell-cell contact growth control was seen in cells that had been transfected with oncogenic Raf-1, and expression levels of occludin and another claudin are lower in these cells (Li & Mrsny (2000) *J. Cell Biol.* 148: 791-800). Occludin expression has been up-regulated *in vitro* by the addition of various fatty acids that have anti-cancer effects, decreasing the paracellular permeability (Jiang *et al.*, (1998) *Biochem. Biophys. Res. Commun.* 244: 414-420). The extreme down-regulation of occludin and claudin-4 in 15 metastatic liver tumors is strongly supported by the reports of tight junction breakdown in tumor tissues.

The present study identified 93 significantly up-regulated genes in both primary HCC and metastatic liver tumors that were not found to have any detectable level of expression in the normal samples. Serine protease inhibitor, Kazal type I (SPINK1), also 20 called pancreatic secretory trypsin inhibitor (PSTI) or tumor-associated trypsin inhibitor (TATI), is one such gene. It is highly expressed in the cells of normal pancreas and in the mucosa of the gastrointestinal tract where it offers protection from proteolytic breakdown. A marked increase in expression is seen in various pancreatic diseases and in tumors of different tissues, including gastric carcinomas, colorectal cancers, and other neoplastic 25 tissues. This increase is presumably due to the elevated expression of trypsin in the tumors, and not related to amplification or rearrangements within the gene. SPINK1 is also considered a valuable marker for a number of solid tumors. A drastic elevation of SPINK1 in the blood of patients with hepatocellular carcinoma has been seen (see Ohmachi *et al.*). Furthermore, it has been suggested that the level of expression correlates with the extent of 30 tumor, such that this heightened expression level could be indicative of HCC under certain conditions. In keeping with this report of overexpression in these tumors, the present expression data show the levels of expression of this gene in HCC samples to be 28.9 times

higher than normal ($P=0.00003$), and in metastatic liver tumors the expression level is 9.8 times higher than normal ($P=0.03697$).

Midkine is one of a family of heparin-binding growth factors, inducible by retinoic acid, and is actively involved in cell-cell interactions and angiogenesis. The expression pattern of midkine is highly restricted in normal adult tissues, and no expression has been reported in normal adult liver, although its expression is required during embryogenesis for normal development. However, it is expressed in moderate to high levels in many tumors, including Wilm's tumors of the kidney, stomach, colon, pancreas, lung, esophagus, breast, and liver tumors. The present data confirm these reports, showing a significant overexpression of midkine in hepatocellular carcinoma samples (fold change 9.9, $P=0.02104$) and in liver metastases (fold change 10.4, $P=0.01818$), but no noticeable expression in normal liver.

Stathmin, leukemia-associated phosphoprotein 18, is a phosphoprotein whose expression pattern and phosphorylation status are controlled by extracellular signals responsible for the regulation of the processes of cell proliferation and differentiation. It is also involved in the regulation of cell division via the destabilization of microtubules. When comparing expression levels between non-malignant tissues and malignant tissues, the tumors generally show a significant up-regulation of this phosphoprotein, specifically lymphomas, leukemias, breast and prostate tumors. One reason proposed for this elevated expression in cancer cells is the dissimilarity in the rates of cell proliferation and states of differentiation between normal and tumor cells. In both HCC samples and metastatic adenocarcinomas, significant up-regulation of stathmin, 9.4 fold in HCC ($P=0.00015$) and 4.8 fold in metastatic tumors ($P=0.00514$) was seen.

Both the genes and ESTs described here will provide valuable information for the identification of new drug targets against liver carcinomas, and that information may be extended for use in the study of carcinogenesis in other tissues.

Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, applications and publications referred to in this application are herein incorporated by reference in their entirety.

Table 1. Clinical Information for Hepatocellular Carcinoma, Metastatic Liver Tumor, and Normal Liver Samples Included in this Study

Sample	Pathology	Primary Tumor	Age	Gender	Race	TNM Classification	Histopathologic Grade	Clinical Stage
HCC1	Hepatocellular Carcinoma	Liver	64	Male	Caucasian	T3,Nx,Mx	G2	stage II
HCC2	Hepatocellular Carcinoma	Liver	27	Female	Caucasian	T3,NO,Mx	G1	stage III
HCC3	Hepatocellular Carcinoma	Liver	78	Female	Caucasian	T4,Nx,Mx	G2	stage III
HCC4	Hepatocellular Carcinoma	Liver	43	Male	Asian	T4,N1,Mx	G2	stage IV
HCC5	Hepatocellular Carcinoma	Liver	51	Male	Caucasian	T4,NO,Mx	G2	stage IV
HCC6	Hepatocellular Carcinoma	Liver	57	Male	Caucasian	unavailable	G2	stage III
M1	Metastatic Adenocarcinoma	Rectum	61	Female	Caucasian	Tx,Nx,M1	G3	stage IV; Duke D
M2	Metastatic Adenocarcinoma	Colon	54	Male	Caucasian	unavailable	G2	stage IV; Duke D
M3	Metastatic Adenocarcinoma	Rectum	50	Female	Caucasian	Tx,Nx,M1	G2	stage IV; Duke D
M4	Metastatic Adenocarcinoma	Colon	60	Male	Caucasian	Tx,Nx,M1	G2	stage IV; Duke D
M5	Metastatic Adenocarcinoma	Colon	57	Male	Caucasian	Tx,Nx,M1	G2	stage IV; Duke D
N1	Normal liver		54	Female	Caucasian			
N2	Normal liver		55	Female	Caucasian			
N3	Normal liver		58	Male	Caucasian			
N4	Normal liver		44	Female	Caucasian			
N5	Normal liver		40	Female	Caucasian			
N6	Normal liver		72	Female	Caucasian			
N7	Normal liver		48	Female	Unknown			
N8	Normal liver		55	Female	Caucasian			

Table 2. Summary of Genes and ESTs Expressed in HCC, Metastatic Liver Tumors, and Normal Livers

	Hepatocellular Carcinoma	Colorectal Metastases	Normal Livers
I. Fingerprint of Gene Expression			
Genes and ESTs commonly expressed in sample set	8479	5102	6213
Genes and ESTs commonly unexpressed in sample set	23233	30455	24800
II. Fold Change			
Genes and ESTs overexpressed in tumors (fold change >3 and p<0.05)	842	1044	
Number of Genes	430	603	
Number of ESTs	412	441	
Genes and ESTs underexpressed in tumors (fold change >3 and p<0.05)	393	1867	
Number of Genes	235	1016	
Number of ESTs	158	851	
III. Differential Comparison between Normal and Tumor Expression			
Genes and ESTs turned ON in tumors	243	286	
Genes and ESTs with expression level above threshold in tumor	77	155	
Number of Genes	38	83	
Number of ESTs	39	72	
Genes and ESTs turned OFF in tumors	47	903	
Genes and ESTs with expression level above threshold in normal	23	449	
Number of Genes	13	289	
Number of ESTs	10	160	

Table 3A. Top fifteen genes overexpressed in hepatocellular carcinoma.

Genbank	Seq ID	Unigene Cluster	Gene Name	Fold Change	Pvalue
AA055896	135	Hs.146428	collagen, type V, alpha 1	10.9*	0.00907
AA156187	339	Hs.81634	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	9.4	0.02007
AA428172	986	Hs.8546	Notch (Drosophila) homolog 3	9.6*	0.00195
AA430032	1009	Hs.252587	pituitary tumor-transforming 1	10.7*	0.00052
AA505133	1417	Hs.279905	solute carrier family 2 (facilitated glucose transporter), member 3	12.2	0.00169
AA610116	1499	Hs.102737	tetraspan NEET-6 protein	16.4	0.00249
AA620881	1510	Hs.21858	trinucleotide repeat containing 3	9.5	0.00062
D31094	1639	Hs.109798	G8 protein	9.4	0.00448
D51276	1678	Hs.81915	leukemia-associated phosphoprotein p18 (stathmin)	9.4	0.00015
J03464	2094	Hs.179573	collagen, type I, alpha 2	10.4	0.00979
M94250	2426	Hs.82045	midkine (neurite growth-promoting factor 2)	9.9*	0.02104
N33920	2493	Hs.44532	diubiquitin	50.3	0
W45320	3523	Hs.228059	KRAB-associated protein 1	10.1*	0.00002
Y00705	3850	Hs.181286	serine protease inhibitor, Kazal type 1	28.9	0.00003
Z37987	3882	Hs.119651	glypican 3	10.7	0.02304

Table 3B. Top fifteen genes underexpressed in hepatocellular carcinoma.

Genbank	Seq ID	Unigene Cluster	Gene Name	Fold Change	Pvalue
AA007395	17	Hs.1219	alcohol dehydrogenase 4 (class II), pi polypeptide	37.8	0.00939
AA010605	26	Hs.2899	4-hydroxyphenylpyruvate dioxygenase	25.5	0.00855
AA448002	1113	Hs.23759	putative type II membrane protein		
H58692	1960	Hs.9520	formyltetrahydrofolate dehydrogenase	14.1*	0
H80901	2005	Hs.272576	ficolin (collagen/fibrinogen domain-containing) 3 (Hakata antigen)	20.2	0.00485
H81070	2006	Hs.8765	RNA helicase-related protein	18.6	0
K03192	2127	Hs/183554	cytochrome P450, subfamily IIA (phenobarital-inducible), polypeptide 6	39.6	0.00002
M29873	2318	Hs.1360	cytochrome P450, subfamily IIB (phenobarital-inducible)	14.2	0.0307
N80129	2703	Hs.94360	metallothionein 1L	17.9	0.01468
R97419	3004	Hs.35718	cytochrome P450, subfamily VIII B (sterol 12-alpha-hydroxylase), polypeptide 1	26.9	0.00999
T48075	3130	Hs.251577	hemoglobin, alpha 1	19.3	0.00807
T67931	3184	Hs.7645	fibrinogen, B beta polypeptide	35.8	0.00471
T95813	3262	Hs.137476	KIAA1051 protein	17.3	0.00128
U56814	3393	Hs.88646	deoxyribonuclease I-like 3	20.4	0.01361
W88946	3639	Hs.18508	putative glycine-N-acetyltransferase	17.7	0.00007
				25.3	0.00221

Table 4A. Top fifteen genes overexpressed in metastatic carcinomas of the liver.

Genbank	Seq ID	Unigene Cluster	Gene Name	Fold Change	Pvalue
				50.9*	0.000831
AA100719	212	Hs.73848	Carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	50.9*	0.000831
AA156243	340	Hs.154737	Serine protease, umbilical endothelium	41.4*	0.00139
AA335191	741	Hs.173724	Creatine kinase, brain	47.4*	0.00419
AA421562	934	Hs.91011	Anterior gradient 2 (<i>Xenopus laevis</i>) homolog	56.3*	0.0041
AA427468	973	Hs.5372	Claudin 4	84.4*	0
AA429009	894	Hs.233950	Serine protease inhibitor, Kunitz type 1	30.0*	0.00001
AA610116	1499	Hs.102737	Tetraspan NET-8 protein		
H58873	1861	Hs.169902	Solute carrier family 2 (facilitated glucose transporter), member 3	58.0*	33.7 0.00171
H94471	2042	Hs.171952	Occludin		0.00063
H95233	2048	Hs.31439	Serine protease inhibitor, Kunitz type, 2	43.1	0
HG2788-HT2896		Hs.27258	Calcyclin binding protein	47.1	0
M29540	2317	Hs.220529	Carcinoembryonic antigen-related cell adhesion molecule 5	33.2	0
M35252	2343	Hs.84072	Transmembrane 4 superfamily member 3	36.6*	0.0116
N92934	2725	Hs.17409	Cysteine-rich protein 1 (intestinal)	39.1	0
X93036	3830	Hs.92323	FXYD domain-containing ion transport regulator 3	35.5	0.002
				42.4*	0.00167

Table 4B. Top fifteen genes underexpressed in metastatic carcinoma of the liver.

Genbank	Seq ID	Unigene Cluster	Gene Name	Fold Change	P value
AA256367	579	Hs.107966	Paraoxonase 3	70.3	0.00192
H58692	1960	Hs.9520	Formyltetrahydrofolate dehydrogenase	81.4*	0
K03192	2127	Hs.183584	Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6	69.9*	0
L16883	2166	Hs.167529	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9	84.7	0.00327
M15656	2268	Hs.234234	Aldolase B, fructose-bisphosphate	96.7*	0
M16594	2272	Hs.89552	Glutathione S-transferase A2	73.2*	0
MB1349	2405	Hs.1955	Serum amyloid A4, constitutive	78.2	0.00015
N53031	2556	Hs.89691	UDP glycosyltransferase 2 family, polypeptide B4	97.6	0.00022
N54417	2567	Hs.90765	Fibrinogen, A alpha polypeptide	99.3	0.00001
R43174	2848	Hs.1898	Paraoxonase 1	74.0*	0.00038
R49459	2882	Hs.63758	Transferin receptor 2	85.6	0.00048
T48039	3129	Hs.2351	Protein C (inactivator of coagulation factors Va and VIIa)	84.4	0.00112
T59148	3158	Hs.50966	Carbamoyl-phosphate synthetase 1, mitochondrial	88.9*	0
U22029	3327	Hs.250615	Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7	72.0*	0
X55283	3734	Hs.1259	Asialoglycoprotein receptor 2	85	0.00084

Table 5. Top fifteen genes expressed in both hepatocellular carcinomas and metastatic liver tumors ad not in normal livers.

Genbank	Seq ID	Unigene Cluster	Gene Name	HCC Fold Change	HCC p value	HCC Fold Change	HCC p value	Metastatic Fold Change	Metastatic p value
AA055896	135	Hs.146428	collagen, type V, alpha 1	10.9	0.00907	18.2	0.00146		
AA204927	425	Hs.77899	tropomyosin 1 (alpha)	6.1	0.0014	7.1	0.00074		
AA335191	741	Hs.173724	creatine kinase, brain	6.5	0.01462	47.4	0.00419		
AA428472	997	Hs.236522	DKFZP434P106 protein	8.8	0.00063	8.3	0.00208		
AA434418	1036	Hs.72172	KIAA1115 protein	6.8	0.0032	5.1	0.00498		
AA452724	1149	Hs.166468	programmed cell death 5	7.7	0.00085	7.2	0.00908		
AA610116	1499	Hs.102737	tetraspant NET-6 protein	16.4	0.00249	33.7	0.00171		
AA620881	1510	Hs.21858	trinucleotide repeat containing 3	9.5	0.00062	8.7	0.00735		
D26129	1635	Hs.78224	ribonuclease, RNase A family, 1 (pancreatic)	6.9	0.00008	5.7	0.03827		
D31094	1639	Hs.109798	G8 protein	9.4	0.0048	4.4	0.04845		
D51276	1678	Hs.81915	leukemia-associated phosphoprotein p18 (stathmin)	9.4	0.00015	4.8	0.00514		
H27188	1908	Hs.9930	collagen-binding protein 2 (collagen 2)	5.8	0.01826	4.2	0.02073		
J03464	2094	Hs.179573	collagen, type I, alpha 2	10.4	0.00979	9.8	0.00028		
M94250	2426	Hs.82045	mildkine (neurite growth-promoting factor 2)	9.9	0.02104	10.4	0.01818		
Y00705	3850	Hs.181286	serine protease inhibitor, Kazal type 1	28.9	0.00003	9.8	0.03697		

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA001409_i_at	AA001409	1 EST	3.35	up	0.04092
rc_AA001504_f_at	AA001504	2 EST	9.98	up	0.00336
rc_AA007158_f_at	AA007158	15 EST	3.05	up	0.01964
rc_AA007160_at	AA007160	16 EST	6	up	0.01035
rc_AA010065_s_at	AA010065	22 CDC28 protein kinase 2	6.25	up	0.02752
rc_AA011134_at	AA011134	29 EST	28.79	up	0.00602
rc_AA011383_at	AA011383	31 EST	5.17	up	0.00008
rc_AA025166_s_at	AA025166	50 fusion, derived from t(12;16) malignant liposarcoma	3.71	up	0.0052
rc_AA025277_at	AA025277	51 EST	4.56	up	0.03136
rc_AA026030_at	AA026030	53 EST	11.01	up	0.01649
rc_AA026092_at	AA026092	54 EST	3.83	up	0.04596
rc_AA026150_at	AA026150	55 EST	5.14	up	0.01072
rc_AA026356_at	AA026356	57 EST	4.1	up	0.00133
rc_AA027946_at	AA027946	60 EST	3.22	up	0.00098
rc_AA028103_at	AA028103	61 EST	3.52	up	0.01142
rc_AA028132_s_at	AA028132	62 EST	6.25	up	0.00646
rc_AA029215_at	AA029215	64 adaptor-related protein complex 2, beta 1 subunit	3.65	up	0.00037
rc_AA029356_at	AA029356	66 EST	3.68	up	0.01545
rc_AA033790_f_at	AA033790	74 apolipoprotein D	4.21	up	0.03247
rc_AA034378_f_at	AA034378	77 endogenous retroviral protease	4.01	up	0.00974
rc_AA034499_s_at	AA034499	78 zinc finger protein 198	3.7	up	0.02143
rc_AA040465_at	AA040465	95 EST	3.25	up	0.00146
rc_AA043959_at	AA043959	101 tropomyosin 4	8.54	up	0.00222
rc_AA053007_f_at	AA053007	123 putative receptor protein	6.76	up	0.00061
rc_AA053033_at	AA053033	124 EST	7.83	up	0.0379
rc_AA053102_s_at	AA053102	125 cadherin 17, L1 cadherin (liver-Intestine)	26.63	up	0.01745
rc_AA053248_l_at	AA053248	126 EST	7.01	up	0.00003
rc_AA053248_f_at	AA053248	126 EST	6.16	up	0.00191
rc_AA053424_at	AA053424	127 EST	8.76	up	0.01775
rc_AA053660_at	AA053660	128 EST	15.98	up	0.00003
rc_AA055805_s_at	AA055805	132 EST	42.83	up	0.00142

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA055811_s_at	AA055811	133	glycoprotein A33 (transmembrane)	6.86	up	0.02152
rc_AA055896_at	AA055896	135	collagen, type V, alpha 1	18.16	up	0.00146
AA056361_at	AA056361	140	integral membrane protein 2C	3.53	up	0.02983
rc_AA062721_at	AA062721	146	nuclear factor (erythroid-derived 2)-like 1	6.2	up	0.00024
rc_AA070206_at	AA070206	155	EST	4.26	up	0.00018
rc_AA070827_at	AA070827	157	EST	4.41	up	0.01902
rc_AA074514_at	AA074514	160	EST	7.69	up	0
rc_AA075299_at	AA075299	164	EST	34.27	up	0.00002
rc_AA075580_f_at:	AA075580	165	EST	4.98	up	0.02083
rc_AA075722_at	AA075722	166	nuclear transport factor 2 (placental protein 15)	4.14	up	0.00374
AA078862_s_at	AA078862	173	EST	6.52	up	0.00025
rc_AA084901_at	AA084901	181	ribosomal protein S6 kinase, 70kD, polypeptide 2	9.13	up	0.00003
rc_AA084921_f_at	AA084921	182	ribosomal protein S10	3.29	up	0.04872
			kangal 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))	5.14	up	0.01916
rc_AA086232_f_at	AA086232	186	DEK oncogene (DNA binding)	5.6	up	0.02551
AA093497_s_at	AA093497	199	EST	3.52	up	0.04805
AA094517_at	AA094517	202	hypothetical 43.2 Kd protein	4.47	up	0.00243
AA094752_at	AA094752	203	EST	29.07	up	0
rc_AA099404_s_at	AA099404	208	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	50.88	up	0.00081
rc_AA100719_s_at	AA100719	212	EST	24.78	up	0
rc_AA101551_at	AA101551	216	tumor suppressing subtransferable candidate 3	10.58	up	0.00543
rc_AA113149_s_at	AA113149	226				
rc_AA113303_at	AA113303	227	transmembrane 4 superfamily member (tetraspan NET-7)	3.73	up	0.00084
rc_AA116036_at	AA116036	233	chromosome 20 open reading frame 1	8.81	up	0.00133
rc_AA121315_at	AA121315	237	KIAA1077 protein	4.86	up	0.02438
rc_AA122386_at	AA122386	239	collagen, type V, alpha 2	4.28	up	0.005
rc_AA126044_at	AA126044	245	EST	11.23	up	0.00041
rc_AA126429_at	AA126429	247	peroxisomal farnesylated protein	3.23	up	0.00478

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA126459_s_at	AA126459	248	DKFZP566B023 protein	3.69	up	0.00352
rc_AA126719_at	AA126719	250	EST	5.31	up	0.00026
AA127712_at	AA127712	255	EST	6.59	up	0.03706
rc_AA127851_at	AA127851	257	EST	3.23	up	0.01943
rc_AA128407_at	AA128407	259	EST	3.78	up	0.01081
rc_AA128561_at	AA128561	261	collagen, type XVII, alpha 1	6.09	up	0.0433
rc_AA131084_at	AA131084	265	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	4.74	up	0.00427
rc_AA131162_s_at	AA131162	266	EST	4.68	up	0.00042
rc_AA131584_at	AA131584	268	DKFZP564O0463 protein	6.83	up	0.00025
rc_AA131894_at	AA131894	269	EST	3.76	up	0.00384
rc_AA131919_at	AA131919	270	putative type II membrane protein	15.36	up	0.00027
rc_AA132032_s_at	AA132032	271	trinucleotide repeat containing 1	4.19	up	0.00295
rc_AA132554_at	AA132554	273	EST	4.96	up	0.02076
rc_AA132983_at	AA132983	274	DKFZP586G1517 protein	3.31	up	0.01155
rc_AA132986_at	AA132986	275	EST	9.72	up	0.00552
rc_AA133590_at	AA133590	282	EST	3.23	up	0.03565
rc_AA133936_at	AA133936	284	EST	9.19	up	0.00088
rc_AA134052_s_at	AA134052	285	Rab geranylgeranyltransferase, alpha subunit	3.54	up	0.03062
rc_AA134158_s_at	AA134158	287	EST	3.42	up	0.0277
rc_AA134968_at	AA134968	289	EST	12.11	up	0.00079
rc_AA134985_at	AA134985	290	EST	12.11	up	0.00318
rc_AA135407_f_at	AA135407	292	endogenous retroviral protease	3.64	up	0.01086
rc_AA135871_at	AA135871	294	EST	3.39	up	0.01544
rc_AA135894_at	AA135894	295	retinoic acid induced 3	14.27	up	0.00558
rc_AA136547_at	AA136547	302	EST	3.51	up	0.00308
rc_AA143493_at	AA143493	310	pleckstrin 2 (mouse) homolog	4.58	up	0.01037
rc_AA143763_at	AA143763	311	EST	18.08	up	0.00347
rc_AA146619_at	AA146619	312	EST	4.87	up	0.00863
rc_AA147084_at	AA147084	314	proliferation-associated 2G4, 38kD	4.4	up	0.0045
rc_AA147439_s_at	AA147439	315	EST	5.01	up	0.00336

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA148885_at	AA148885	320	minichromosome maintenance deficient (<i>S. cerevisiae</i>) 4	6.39	up	0.0125
rc_AA148977_at	AA148977	322	EST	3.64	up	0.02911
rc_AA149889_at	AA149889	326	neighbor of A-kinase anchoring protein 95	3.34	up	0.02054
rc_AA150053_at	AA150053	327	EST	3.71	up	0.00102
rc_AA151182_at	AA151182	332	EST	3.51	up	0.00043
rc_AA151428_s_at	AA151428	335	matrix metalloproteinase 23B	7.15	up	0.00056
rc_AA161778_at	AA161778	338	claudin 7	5.77	up	0.00002
rc_AA156187_at	AA156187	339	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit b, isoform 1	23.24	up	0.00006
rc_AA156243_at	AA156243	340	serine protease, umbilical endothelium	41.44	up	0.00139
rc_AA156450_at	AA156450	342	EST	3.33	up	0.00587
rc_AA157818_f_at	AA157818	349	endogenous retroviral protease	25.99	up	0.00153
rc_AA158234_at	AA158234	351	EST	17.04	up	0.00711
rc_AA158795_at	AA158795	352	EST	3.07	up	0.00057
rc_AA159525_at	AA159525	354	EST	49.39	up	0.00062
rc_AA161043_at	AA161043	356	tetraspan 1	18.8	up	0.00015
rc_AA161292_s_at	AA161292	357	interferon, alpha-inducible protein 27	13.84	up	0.00004
rc_AA164252_f_at	AA164252	358	VGF nerve growth factor inducible NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD)	3.41	up	0.00154
rc_AA169837_at	AA169837	364	(NADH-coenzyme Q reductase)	3.17	up	0.03038
rc_AA171760_at	AA171760	367	EST	17.86	up	0
rc_AA171939_at	AA171939	368	EST	4.67	up	0.00104
rc_AA172076_at	AA172076	369	EST	3.06	up	0.00326
rc_AA173430_at	AA173430	371	EST	4.32	up	0.04362
rc_AA179298_at	AA179298	378	stomatin-like protein 2	3.72	up	0.00299
rc_AA179787_at	AA179787	380	polyglutamine binding protein 1	6.44	up	0.00206
rc_AA179845_at	AA179845	381	EST	5.77	up	0.01414
rc_AA181600_at	AA181600	384	EST	5.38	up	0.03316
rc_AA182001_i_at	AA182001	386	EST	3.56	up	0.00945
rc_AA187938_at	AA187938	391	EST	3.86	up	0.00512

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA188378_j_at	AA188378	392	EST	9.56	up	0.00271
rc_AA188378_f_at	AA188378	392	EST	5.54	up	0.01359
rc_AA189015_at	AA189015	394	EST	5.27	up	0.00004
rc_AA1911708_at	AA1911708	400	EST	3.87	up	0.01904
rc_AA192755_at	AA192755	401	EST	3.13	up	0.00442
rc_AA194237_at	AA194237	408	EST	3.13	up	0.00212
rc_AA194724_at	AA194724	409	endonuclease G	3.09	up	0.04011
rc_AA196790_at	AA196790	421	EST	7.64	up	0.00287
rc_AA204927_at	AA204927	425	tropomyosin 1 (alpha)	7.09	up	0.00074
rc_AA211483_at	AA211483	435	EST	44.07	up	0.00175
rc_AA211851_f_at	AA211851	436	EST	3.66	up	0.00789
rc_AA213696_at	AA213696	437	poly(A)-binding protein, cytoplasmic 1	24.65	up	0.00001
AA215299_s_at	AA215299	439	L6 snRNA-associated Sm-like protein LSm7	15.84	up	0.00001
rc_AA215468_s_at	AA215468	441	ADP-ribosylation factor-related protein 1	3.9	up	0.04549
rc_AA218663_at	AA218663	444	acid-inducible phosphoprotein	3.26	up	0.03537
AA224502_at	AA224502	451	EST	4.12	up	0.00694
rc_AA226932_at	AA226932	453	DKFZP564F0923 protein	6.84	up	0.00405
rc_AA227560_at	AA227560	458	EST	12.81	up	0.01693
rc_AA227926_at	AA227926	460	EST	6.81	up	0.01701
rc_AA233886_s_at	AA233886	475	D site of albumin promoter (albumin D-box) binding protein	3.38	up	0.0218
rc_AA233959_i_at	AA233959	477	EST	19.69	up	0.00101
rc_AA234096_at	AA234096	479	EST	23.72	up	0.00018
rc_AA234362_at	AA234362	481	EST	3.89	up	0.03524
rc_AA235707_at	AA235707	500	EST	9.17	up	0.00005
rc_AA236037_at	AA236037	506	EST	5.74	up	0.0091
rc_AA236533_s_at	AA236533	514	ecotropic viral integration site 1	4.01	up	0.02882
rc_AA236714_f_at	AA236714	516	nuclear mitotic apparatus protein 1	4.35	up	0.00083
rc_AA237017_at	AA237017	521	KIAA1068 protein	3.52	up	0.00976
rc_AA243133_at	AA243133	525	serine/threonine kinase 15	7.73	up	0.04328
rc_AA243173_at	AA243173	526	EST	8.75	up	0.00003

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
AA249819_s_at	AA249819	535	EST	5.09	up	0.00136
rc_AA251230_at	AA251230	540	EST	4.75	up	0.00054
rc_AA251299_s_at	AA251299	541	KIAA0014 gene product	16.86	up	0.00046
rc_AA251909_at	AA251909	549	EST	3.35	up	0.03937
rc_AA252994_at	AA252994	557	apoptosis inhibitor 4 (survivin)	3.55	up	0.00075
rc_AA253011_f_at	AA253011	558	KIAA0713 protein	4.73	up	0.01944
AA253330_s_at	AA253330	562	adaptor-related protein complex 1, gamma 1 subunit	3.87	up	0.00708
rc_AA253473_at	AA253473	567	EST	15.23	up	0.00171
rc_AA256273_at	AA256273	577	EST	4.13	up	0.03874
rc_AA256642_at	AA256642	582	EST	11.17	up	0.00035
rc_AA258482_s_at	AA258482	596	Zinc finger protein	3.17	up	0.04606
rc_AA261907_at	AA261907	603	DKFZP566E144 protein	4.54	up	0.02289
rc_AA262477_at	AA262477	608	ribonuclease HI, large subunit	4.87	up	0.00005
rc_AA262887_at	AA262887	610	EST	5.4	up	0.04719
rc_AA262943_at	AA262943	611	EST	13.42	up	0.00234
rc_AA262969_f_at	AA262969	613	ferritin, heavy polypeptide 1	4.49	up	0.00013
AA263044_s_at	AA263044	615	H2A histone family, member Y	4.13	up	0.00024
rc_AA278817_at	AA278817	618	EST	4.22	up	0.00061
rc_AA278838_s_at	AA278838	620	EST	3	up	0.02832
rc_AA279177_at	AA279177	624	lymphocyte antigen 75	6.05	up	0.01821
rc_AA279840_at	AA279840	632	tillin-cap (telethonin)	5.58	up	0.01253
rc_AA280283_s_at	AA280283	637	EST	4.99	up	0.02644
rc_AA280734_l_at	AA280734	639	KIAA0618 gene product	9.64	up	0.00003
rc_AA280928_at	AA280928	642	EST	3.27	up	0.04625
rc_AA282149_s_at	AA282149	654	huntingtin interacting protein-1-related	4.19	up	0.00091
rc_AA282247_at	AA282247	657	EST	8	up	0.00014
rc_AA283085_s_at	AA283085	667	EST	4.93	up	0.00382
rc_AA284879_at	AA284879	679	EST	24.68	up	0.00001
rc_AA284945_at	AA284945	680	EST	5.98	up	0.00026
rc_AA287022_s_at	AA287022	685	thymidine kinase 1, soluble	4.51	up	0.02582
rc_AA287347_at	AA287347	687	EST	5.47	up	0.00034

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
		688	EST	5.68	up	0.00062
rc_AA287393_at	AA290674	692	eukaryotic translation initiation factor 4E binding protein 1	11.59	up	0.00036
rc_AA291137_at	AA291137	694	EST	5.21	up	0.00685
rc_AA291139_at	AA291139	695	EST	8.69	up	0.04573
rc_AA291168_at	AA291168	696	EST	40.67	up	0.00065
AA291456_s_at	AA291456	700	EST	3.96	up	0.03633
rc_AA291659_at	AA291659	702	EST	3.83	up	0.01934
rc_AA292379_at	AA292379	708	EST	6.04	up	0.00568
rc_AA292659_at	AA292659	710	EST	3.48	up	0.00037
rc_AA292765_at	AA292765	712	ZW10 interactor	7.14	up	0.02623
rc_AA292788_s_at	AA292788	714	EST	7.69	up	0.00867
rc_AA292931_at	AA292931	715	EST	3.97	up	0.00067
rc_AA293719_at	AA293719	720	EST	4.69	up	0.02181
AA295819_s_at	AA295819	722	EST	8	up	0.01793
AA298786_at	AA298786	727	EST	4.65	up	0.02821
AA306121_at	AA306121	729	EST	4.85	up	0.00381
AA307748_s_at	AA307748	730	EST	3.7	up	0.00001
AA320369_s_at	AA320369	735	chromosome 19 open reading frame 3	4.33	up	0.00554
AA328993_s_at	AA328993	738	EST	3.66	up	0.00146
rc_AA331393_at	AA331393	739	EST	16.73	up	0.00848
rc_AA335091_at	AA335091	740	EST	5.28	up	0.0009
rc_AA335191_f_at	AA335191	741	creatine kinase, brain	47.35	up	0.00419
rc_AA338729_at	AA338729	743	EST	3.33	up	0.00046
rc_AA338889_f_at	AA338889	745	actin related protein 2/3 complex, subunit 4 (20 kD)	10.77	up	0.03782
AA364267_at	AA364267	762	EST	5.01	up	0.00255
rc_AA370163_at	AA370163	766	EST	3.34	up	0.00643
rc_AA372018_at	AA372018	768	EST	14.3	up	0.00178
AA372630_s_at	AA372630	769	differentially expressed in hematopoietic lineages	25.49	up	0.01743
AA384184_s_at	AA384184	774	DkFZP586B0519 protein	3.38	up	0.01209
rc_AA394121_at	AA394121	778	laminin receptor 1 (67kD, ribosomal protein SA)	23.78	up	0.00099

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P-value
rc_AA397906_at	AA397906	782	DKFZP434I216 protein	3.2	up	0.00138
rc_AA397916_f_at	AA397916	784	EST	3.27	up	0.02895
rc_AA398205_at	AA398205	789	EST	4.17	up	0.00004
rc_AA398761_s_at	AA398761	799	EST	3.43	up	0.00726
rc_AA398908_at	AA398908	801	EST	38.69	up	0.01089
rc_AA399226_at	AA399226	803	tight junction protein 3 (zona occludens 3)	3.59	up	0.02002
rc_AA400271_at	AA400271	814	EST	3.51	up	0.00742
rc_AA401958_at	AA401958	832	EST	3.62	up	0.01232
rc_AA402495_at	AA402495	838	EST	4.91	up	0.00235
AA402937_at	AA402937	843	EST	3.11	up	0.00182
rc_AA402968_at	AA402968	844	EST	3.1	up	0.00453
rc_AA403159_at	AA403159	845	Ste-20 related kinase	7.33	up	0.00187
rc_AA404338_at	AA404338	849	EST	10.9	up	0.00668
rc_AA405310_at	AA405310	856	EST	3.23	up	0.00138
rc_AA405460_at	AA405460	857	EST	4.02	up	0.03492
rc_AA405715_at	AA405715	862	hypothetical protein	4.68	up	0.00898
rc_AA405791_at	AA405791	864	EST	21.22	up	0
rc_AA406145_f_at	AA406145	870	EST	6.71	up	0.00047
rc_AA406218_at	AA406218	872	EST	4.88	up	0.02194
rc_AA406385_at	AA406385	876	DKFZP564B0769 protein	3.21	up	0.00724
rc_AA406542_at	AA406542	878	EST	8.27	up	0.00023
rc_AA410469_at	AA410469	883	EST	6.3	up	0.00103
rc_AA410508_at	AA410508	885	EST	16.04	up	0.02635
rc_AA410962_s_at	AA410962	887	peroxisome proliferative activated receptor, delta	3.45	up	0.04574
rc_AA410972_at	AA410972	888	EST	3.12	up	0.00023
rc_AA411502_at	AA411502	889	EST	16.42	up	0.00241
rc_AA411685_at	AA411685	890	EST	3.83	up	0.00417
rc_AA411813_at	AA411813	893	postmeliotic segregation increased 2-like 1	6.76	up	0.03499
rc_AA412301_at	AA412301	899	EST	4.57	up	0.00026
rc_AA412403_at	AA412403	900	EST	3.09	up	0.00047
rc_AA412405_s_at	AA412405	901	EST	13.82	up	0.01021

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA412720_at	AA412720	905	EST	3.6	up	0.01396
rc_AA416963_at	AA416963	911	EST	3.69	up	0.03956
rc_AA416973_at	AA416973	913	EST	3.61	up	0.0091
rc_AA419217_at	AA419217	923	DKFZP586E1422 protein	0.00045		
rc_AA421562_at	AA421562	934	anterior gradient 2 (<i>Xenopus laevis</i>) homolog	0.0041		
rc_AA421638_at	AA421638	935	EST	0.00487		
rc_AA422049_at	AA422049	937	EST	0.0067		
rc_AA422086_at	AA422086	938	EST	0.03418		
rc_AA422150_at	AA422150	939	cytochrome P540 family member predicted from ESTs	0.00108		
rc_AA424029_at	AA424029	943	EST	8.68	up	0.00081
rc_AA424487_at	AA424487	945	EST	38.41	up	0.00002
rc_AA424881_at	AA424881	949	EST	6.3	up	0.00556
rc_AA425279_at	AA425279	951	quiescin Q6	6.15	up	0.00083
rc_AA425401_at	AA425401	954	serine/threonine kinase 24 (Ste20, yeast homolog)	3.22	up	0.00625
rc_AA425852_s_at	AA425852	958	EST	7.78	up	0.00239
rc_AA425852_l_at	AA425852	958	EST	4.8	up	0.03874
rc_AA426447_at	AA426447	965	EST	4.23	up	0.0309
rc_AA426521_at	AA426521	967	Sjogren's syndrome nuclear autoantigen 1	3.47	up	0.01161
rc_AA427442_at	AA427442	971	guanine nucleotide regulatory factor	3.43	up	0.01547
AA427468_s_at	AA427468	973	claudin 4	84.43	up	0
rc_AA427636_at	AA427636	976	EST	19.23	up	0.00145
rc_AA427825_at	AA427825	981	EST	3.32	up	0.01615
rc_aa427925_s_at	AA427925	982	EST	3.23	up	0.01806
rc_AA427946_at	AA427946	983	dynein, axonemal, light polypeptide 4	0.00001		
AA428172_f_at	AA428172	986	Notch (<i>Drosophila</i>) homolog 3	9.53	up	0.02562
rc_AA428964_at	AA428964	993	kallikrein 10	21.83	up	0.02324
rc_AA429009_at	AA429009	994	serine protease inhibitor, Kunitz type 1	30.04	up	0.00001
rc_AA429470_at	AA429470	996	EST	3.67	up	0.00782
rc_AA429472_at	AA429472	997	DKFZP434P106 protein	8.27	up	0.00208
rc_AA429636_at	AA429636	1001	hexokinase 2	10.43	up	0.00597
AA429825_at	AA429825	1003	DKFZP566B023 protein	6.63	up	0.00032

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA429890_s_at	AA429890	1004	cisplatin resistance associated	12.51	up	0.00053
rc_AA430032_at	AA430032	1009	pituitary tumor-transforming 1	16.87	up	0.00659
rc_AA430048_at	AA430048	1012	KIAA0160 protein	6.27	up	0.00631
rc_AA430674_at	AA430674	1018	EST	15.11	up	0.00293
rc_AA431719_at	AA431719	1025	EST	4.25	up	0.00015
rc_AA431776_at	AA431776	1027	EST	3.24	up	0.01814
rc_AA431873_at	AA431873	1028	EST	4.03	up	0.00785
rc_AA432162_at	AA432162	1029	DKFZP586B2022 protein	3.48	up	0.03851
rc_AA433930_at	AA433930	1032	chondroitin 4-sulfotransferase	7.68	up	0.02445
rc_AA434418_at	AA434418	1036	KIAA1115 protein	5.12	up	0.00498
rc_AA435526_s_at	AA435526	1037	transferrin receptor (p90, CD71)	3.69	up	0.00139
rc_AA435665_at	AA435665	1040	EST	8.66	up	0.00001
rc_AA436027_at	AA436027	1050	EST	3.71	up	0.03676
rc_AA436473_s_at	AA436473	1052	EST	3.03	up	0.00133
rc_AA436616_at	AA436616	1056	EST	3.18	up	0.04402
rc_AA437368_at	AA437368	1063	EST	3.75	up	0.01317
rc_AA437387_s_at	AA437387	1064	EST	3.81	up	0.01478
rc_AA441911_at	AA441911	1066	EST	6.14	up	0.00003
AA442054_s_at	AA442054	1067	phospholipase C, gamma 1 (formerly subtype 148)	16.89	up	0.00205
rc_AA442763_at	AA442763	1072	cyclin B2	5.09	up	0.02168
rc_AA443271_at	AA443271	1073	KIAA0546 protein	3.6	up	0.01228
rc_AA443316_s_at	AA443316	1075	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	4.13	up	0.01729
rc_AA443941_at	AA443941	1085	tumor suppressing subtransferable candidate 1	3.57	up	0.01685
rc_AA446949_at	AA446949	1096	EST	3.41	up	0.03411
rc_AA446968_at	AA446968	1097	EST	3.45	up	0.02232
rc_AA447118_s_at	AA447118	1099	EST	3.03	up	0.01702
rc_AA447687_at	AA447687	1104	EST	11.42	up	0.00362
rc_AA447732_at	AA447732	1105	EST	3.2	up	0.00591
rc_AA447991_at	AA447991	1112	EST	4.99	up	0.00173
rc_aa449073_s_at	AA449073	1117	EST	6.89	up	0.01445
rc_AA449122_at	AA449122	1119	EST	3.65	up	0.00369

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
rc_AA449456_at	AA449456	1126	EST	6.28	up	0.00087
rc_AA449458_at	AA449458	1127	EST	3.22	up	0.03098
rc_AA449475_at	AA449475	1128	EST	3.06	up	0.00291
rc_AA449479_at	AA449479	1129	EST	3.09	up	0.03495
rc_AA450247_at	AA450247	1133	EST	5.27	up	0.02833
rc_AA451676_at	AA451676	1135	EST	14.72	up	0.00056
rc_AA451680_at	AA451680	1136	hepatocellular carcinoma associated protein; breast cancer associated gene 1	3.55	up	0.00708
rc_AA451877_at	AA451877	1138	EST	8.63	up	0.00489
rc_AA452259_at	AA452259	1143	EST	3.49	up	0.00114
rc_AA452536_at	AA452536	1145	v-ras simian leukemia viral oncogene homolog A (ras related) programmed cell death 5	5.6	up	0.00481
rc_AA452724_at	AA452724	1149	X-prolyl aminopeptidase (aminopeptidase P)-like	7.2	up	0.00908
rc_AA453477_at	AA453477	1153	EST	4.23	up	0.0001
rc_AA453783_s_at	AA453783	1158	EST	6.16	up	0.00167
rc_AA454597_s_at	AA454597	1166	EST	3.63	up	0.0067
rc_AA454710_at	AA454710	1168	EST	3.42	up	0.00653
rc_AA454908_s_at	AA454908	1171	KIAA0144 gene product	9.3	up	0.00539
rc_AA455521_s_at	AA455521	1178	E2F transcription factor 5, p130-binding	4.6	up	0.00773
rc_AA455522_s_at	AA455522	1179	EST	3.83	up	0.00017
rc_aa458852_f_at	AA458852	1203	KIAA0440 protein	3.2	up	0.00038
rc_AA458890_at	AA458890	1206	EST	3.36	up	0.00303
rc_AA459254_at	AA459254	1211	EST	5.36	up	0.0259
rc_AA459310_r_at	AA459310	1214	EST	3.45	up	0.00179
rc_AA459388_s_at	AA459388	1215	copine I	5.23	up	0.00691
rc_AA459703_at	AA459703	1222	v-myc avian myelocytomatosis viral oncogene homolog	4.75	up	0.02413
rc_AA459961_at	AA459961	1223	EST	3.24	up	0.00316
rc_AA460017_l_at	AA460017	1225	EST	10.76	up	0.00106
rc_AA460017_f_at	AA460017	1225	EST	3.61	up	0.00109
rc_AA461187_at	AA461187	1236	EST	8.15	up	0.00068

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA461473_at	AA461473	1242	nebulette	3.35	up	0.03855
rc_AA461476_at	AA461476	1243	EST	4.12	up	0.00871
rc_AA463234_at	AA463234	1246	KIAA0792 gene product	5.94	up	0.01182
rc_AA463725_at	AA463725	1249	mannosyl (alpha-1,6-) glycoprotein beta-1,2-N-acetylglucosaminyltransferase	7.4	up	0.04715
rc_AA463861_at	AA463861	1251	EST	24.79	up	0.00096
rc_AA464414_at	AA464414	1258	EST	4.99	up	0.00529
rc_AA464698_at	AA464698	1262	EST	3.24	up	0.04854
rc_AA464963_at	AA464963	1265	EST	5.01	up	0.00107
AA471278_at	AA471278	1277	BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog	5.14	up	0.00873
rc_AA476216_at	AA476216	1279	EST	4.97	up	0.00359
rc_AA478017_at	AA478017	1295	zyxin	5.77	up	0.00484
rc_AA478300_at	AA478300	1298	CD39-like 2	6.15	up	0.01625
rc_AA478415_at	AA478415	1299	EST	4.56	up	0.00095
rc_AA478599_at	AA478599	1304	G protein-coupled receptor 56	3.31	up	0.00182
rc_AA479044_s_at	AA479044	1307	EST	6.9	up	0.04668
rc_AA479727_s_at	AA479727	1315	EST	6.06	up	0.00389
rc_AA479797_at	AA479797	1316	EST	7.93	up	0.00006
rc_AA479945_s_at	AA479945	1319	plakophilin 3	3.17	up	0.01767
rc_AA482007_at	AA482007	1331	EST	3.49	up	0.00167
rc_AA482127_at	AA482127	1333	Cdc42Hs	4.88	up	0.00017
rc_AA482224_f_at	AA482224	1334	putative type II membrane protein	4.62	up	0.0105
AA482319_f_at	AA482319	1335	putative type II membrane protein	5.11	up	0.00177
rc_AA482546_s_at	AA482546	1336	KIAA0124 protein	4.41	up	0.00604
rc_AA482613_at	AA482613	1338	DKFZP434B203 protein	4.14	up	0.00186
rc_AA485405_at	AA485405	1343	EST	5.35	up	0.03475
rc_AA485697_at	AA485697	1346	EST	14.74	up	0.00102
rc_AA488987_s_at	AA488987	1365	synaptogyrin 2	3.24	up	0.01444
rc_AA4889707_at	AA4889707	1371	EST	3.47	up	0.03433

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA489712_at	AA489712	1372	EST	4.93	up	0.00726
rc_AA490212_at	AA490212	1375	H2A histone family, member Y	3.71	up	0.01226
rc_AA490494_at	AA490494	1377	EST	5.16	up	0.01696
rc_AA491223_at	AA491223	1389	EST	3.03	up	0.00557
rc_AA496204_at	AA496204	1397	EST	3.69	up	0.01097
rc_AA496245_at	AA496245	1398	EST	3.96	up	0.0039
rc_AA496981_at	AA496981	1404	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog	4.93	up	0.01096
rc_AA497031_at	AA497031	1407	EST	11.05	up	0.04381
rc_AA504111_at	AA504111	1409	EST	3.2	up	0.00544
rc_AA504264_at	AA504264	1410	EST	3.81	up	0.00684
rc_AA504270_at	AA504270	1411	EST	4.96	up	0.01919
AA504413_at	AA504413	1413	EST	3.35	up	0.00079
rc_AA504806_at	AA504806	1416	EST	3.54	up	0.00221
rc_AA598405_at	AA598405	1424	membrane interacting protein of RGS16	4.69	up	0.0122
rc_AA598506_s_at	AA598506	1430	KIAA0179 protein	3.17	up	0.01694
rc_AA598712_at	AA598712	1436	EST	3.03	up	0.03656
rc_AA598988_at	AA598988	1442	EST	4.32	up	0.00044
rc_AA599244_at	AA599244	1448	KIAA0530 protein	3.39	up	0.01246
rc_AA599522_f_at	AA599522	1452	squamous cell carcinoma antigen recognised by T cells	6.75	up	0.04229
rc_AA608579_s_at	AA608579	1464	paired-like homeodomain transcription factor 2	4.29	up	0.04435
rc_AA608897_at	AA608897	1473	EST	9.92	up	0.00087
rc_AA608965_at	AA608965	1474	Hermansky-Pudlak syndrome	3.19	up	0.00204
rc_AA609008_at	AA609008	1475	EST	3.46	up	0.02935
rc_AA609013_s_at	AA609013	1477	dipeptidase 1 (renal)	10.17	up	0.00109
rc_AA609614_at	AA609614	1487	EST	6.5	up	0.00406
rc_AA609786_s_at	AA609786	1491	nucleolar protein 1 (120kD)	4.75	up	0.00261
rc_AA610053_at	AA610053	1496	EST	7.01	up	0.00003
rc_AA610116_l_at	AA610116	1499	tetraspan NET-6 protein	33.68	up	0.00171
rc_AA620466_at	AA620466	1502	EST	5.14	up	0.00004

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA620881_at	AA620881	1510	trinucleotide repeat containing 3	8.66	up	0.00735
rc_AA620995_at	AA620995	1512	EST	3.74	up	0.03414
rc_AA621277_at	AA621277	1520	EST	3.81	up	0.00194
rc_AA621780_at	AA621780	1530	CGI-96 protein	3.65	up	0.01582
AB000584_at	AB000584	1533	prostate differentiation factor	4.7	up	0.00071
AB002533_at	AB002533	1539	karyopherin alpha 4 (importin alpha 3)	6.38	up	0.00003
AB006781_s_at	AB006781	1540	lectin, galactoside-binding, soluble, 4 (galectin 4)	7.05	up	0.00913
AF001294_at	AF001294	1544	tumor suppressing subtransferable candidate 3	7.45	up	0.00009
AF003521_at	AF003521	1545	jagged 2	11.26	up	0.00008
AF004709_at	AF004709	1547	mitogen-activated protein kinase 13	3.92	up	0.00009
C00021_s_at	C00021	1551	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4	3.33	up	0.00215
C01766_s_at	C01766	1559	EST	13.67	up	0.00003
rc_C13692_f_at	C13692	1564	EST	6.39	up	0.00059
rc_C14051_f_at	C14051	1565	phosphoprotein enriched in astrocytes 15	3.68	up	0.01453
rc_C14098_f_at	C14098	1566	EST	3.53	up	0.04401
rc_C14348_at	C14348	1568	EST	4.06	up	0.00111
C14412_s_at	C14412	1569	HSPC038 protein	3.9	up	0.00036
rc_C14756_f_at	C14756	1570	MLN51 protein	5.36	up	0.00001
rc_C15324_f_at	C15324	1574	EST	5.22	up	0.00344
rc_C21248_at	C21248	1585	pituitary tumor-transforming 1	3.85	up	0.00456
D00017_at	D00017	1587	annexin A2	11.38	up	0
D11086_at	D11086	1595	interleukin 2 receptor, gamma (severe combined immunodeficiency)	5.61	up	0.00873
D13413_mna1_s_at	D13413	1604	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	4.79	up	0.00092
D13639_at	D13639	1607	cyclin D2	7.49	up	0.01641
D14520_at	D14520	1613	basic transcription element binding protein 2	4.93	up	0.00004
D14530_at	D14530	1614	ribosomal protein S23	3.1	up	0.00331
D14657_at	D14657	1615	KIAA0101 gene product	3.7	up	0.04079
rc_D19737_at	D19737	1623	golgi autoantigen, golgin subfamily a, 3	3.44	up	0.02212

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P-value
rc_D20464_at	D20464	1625	bromodomain adjacent to zinc finger domain, 2B	3.27	up	0.04897
rc_D20906_at	D20906	1627	EST	5.18	up	0.02189
D21063_at	D21063	1628	minichromosome maintenance deficient (<i>S. cerevisiae</i>) 2	3.83	up	0.00983
D21261_at	D21261	1629	(mitotin)	3.46	up	0.00685
D23660_at	D23660	1630	transgelin 2	3.22	up	0.00316
D25216_at	D25216	1631	ribosomal protein L4	3.17	up	0.02125
D25274_at	D25274	1632	KIAA0014 gene product	3.39	up	0.00238
D25328_at	D25328	1633	EST	3.17	up	0.04925
rc_D25560_I_at	D25560	1634	phosphofructokinase, platelet	4.72	up	0.00661
D26129_at	D26129	1635	ribonuclease, RNase A family, 1 (pancreatic)	5.68	up	0.03827
D28124_at	D28124	1636	neuroblastoma candidate region, suppression of tumorigenicity	6.38	up	0.00015
D31094_at	D31094	1639	1	4.41	up	0.04845
D31417_at	D31417	1645	G8 protein	4.56	up	0.00014
D38073_at	D38073	1651	secreted protein of unknown function	3.65	up	0.01869
D38548_at	D38548	1655	minichromosome maintenance deficient (<i>S. cerevisiae</i>) 3	4.5	up	0.00036
D38583_at	D38583	1656	KIAA0076 gene product	18.7	up	0.00003
D42085_at	D42085	1658	S100 calcium-binding protein A11 (calgizzarin)	3.83	up	0.00036
D43949_at	D43949	1659	KIAA0095 gene product	3.32	up	0.0014
D43950_at	D43950	1660	chaperonin containing TCP1, subunit 5 (epsilon)	3.61	up	0.00672
D49400_at	D49400	1667	ATPase, vacuolar, 14 kD	4.01	up	0.00287
D50663_at	D50663	1671	t-complex-associated-testis-expressed 1-like 1	4.09	up	0.00208
D50913_at	D50913	1672	KIAA0123 protein	3.32	up	0.01202
D50914_at	D50914	1673	KIAA0124 protein	4.74	up	0.00752
rc_D51112_s_at	D51112	1675	collapsin response mediator protein 1	10.48	up	0.00076
rc_D51133_f_at	D51133	1676	tubulin, beta, 4	4.84	up	0.02875
rc_D51276_f_at	D51276	1678	leukemia-associated phosphoprotein p18 (stathmin)	4.81	up	0.00514
rc_D51287_f_at	D51287	1680	ribosomal protein S12	3.3	up	0.02829
rc_D51393_f_at	D51393	1681	ribosomal protein L4	5.64	up	0.00074

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_D52632_f_at	D52632	1683	ribosomal protein S6	3.12	up	0.00498
rc_D53139_f_at	D53139	1684	ribosomal protein S28	4.38	up	0.0009
rc_D54296_f_at	D54296	1685	KIAA0255 gene product	3.8	up	0.01059
D55716_at	D55716	1686	minichromosome maintenance deficient (<i>S. cerevisiae</i>) 7	6.6	up	0.00151
rc_D57489_at	D57489	1689	chaperonin containing TCP1, subunit 7 (eta)	4.08	up	0.00001
rc_D59322_f_at	D59322	1694	EST	4.18	up	0.00006
rc_D59847_at	D59847	1701	EST	3.09	up	0.02206
rc_D60811_s_at	D60811	1704	EST	3.22	up	0.0098
D63391_at	D63391	1710	platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD)	3.91	up	0.00062
D63486_at	D63486	1712	KIAA0152 gene product	6.33	up	0.00078
D63487_at	D63487	1713	KIAA0153 protein	5.4	up	0.00027
D63874_at	D63874	1714	high-mobility group (nonhistone chromosomal) protein 1	3.64	up	0.00228
D63880_at	D63880	1715	KIAA0159 gene product	4.26	up	0.00253
D78361_at	D78361	1718	EST	3.14	up	0.00023
D78676_at	D78676	1719	EST	3.2	up	0.00635
D79205_at	D79205	1721	ribosomal protein L39	3.07	up	0.00021
rc_D80237_s_at	D80237	1729	actin related protein 2/3 complex, subunit 4 (20 kD)	3.27	up	0.00137
rc_D80662_s_at	D80662	1733	adaptor-related protein complex 1, gamma 2 subunit	3.43	up	0.00108
rc_D80710_f_at	D80710	1734	integral type I protein	7.08	up	0.00213
rc_D80917_f_at	D80917	1736	KIAA0670 protein/actinus	3.58	up	0.00007
rc_D80946_f_at	D80946	1737	SFRS protein kinase 1	8.53	up	0.00455
D82348_at	D82348	1744	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	3.93	up	0.00037
D82558_at	D82558	1746	novel centrosomal protein RanBP M	5.94	up	0.00752
D83735_at	D83735	1747	calponin 2	10.42	up	0.00001
D83783_at	D83783		trinucleotide repeat containing 11 (THR-associated protein, 230 kDa subunit)	6.65	up	0.00176

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
D83783_at	D83783	trinucleotide repeat containing 11 (THR-associated protein, 230 kDa subunit)	3.33	up	0.00748
D86956_at	D86956	heat shock 105kD	4	up	0.03013
D86974_at	D86974	KIAA0220 protein	3.85	up	0.0161
D87735_at	D87735	ribosomal protein L14	3.92	up	0.00015
D87953_at	D87953	N-myc downstream regulated	6.12	up	0.00033
D88154_at	D88154	villin-like	4.18	up	0.00051
rc_F01444_f_at	F01444	KIAA0440 protein	6.78	up	0.00028
rc_F01568_at	F01568	EST	3.24	up	0.0018
rc_F02800_at	F02800	EST	3.45	up	0.03238
rc_F02863_at	F02863	EST	3.21	up	0.01039
rc_F04320_s_at	F04320	replication factor C (activator 1) 4 (37kD)	3.63	up	0.01119
rc_F04444_at	F04444	EST	4.57	up	0.01132
rc_F04531_s_at	F04531	Kell blood group precursor (McLeod phenotype)	7.79	up	0.03205
rc_F04674_at	F04674	KIAA0746 protein	8.2	up	0.00028
rc_F09297_s_at	F09297	EST	3.94	up	0.0016
rc_F09394_s_at	F09394	KIAA0715 protein	22.89	up	0.07753
rc_F09684_at	F09684	EST	3.78	up	0.02277
rc_F09788_at	F09788	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	4.14	up	0.00003
rc_F13809_f_at	F13809	tropomyosin 1 (alpha)	7.62	up	0.00012
rc_H04753_f_at	H04753	EST	3.38	up	0.02447
rc_H04799_at	H04799	EST	3.71	up	0.04109
rc_H05394_f_at	H05394	KIAA0266 gene product	4.06	up	0.0015
rc_H05525_s_at	H05525	hypothetical protein	4.6	up	0.0033
rc_H05625_f_at	H05625	EST	5.17	up	0.04551
rc_H08863_at	H08863	hypothetical protein	3.48	up	0.00205
rc_H09241_s_at	H09241	EST	4.17	up	0.00727
rc_H09271_f_at	H09271	EST	5.06	up	0.0016
rc_H09281_at	H09281	EST	6	up	0.00966
rc_H13532_f_at	H13532	ribosomal protein L18a	3.97	up	0.00061

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_H17476_at	H17476	1889	EST	3.44	up	0.00479
rc_H18412_s_at	H18412	1890	isocitrate dehydrogenase 3 (NAD ⁺) gamma	4.37	up	0.00262
rc_H18442_f_at	H18442	1891	creatine kinase, brain	17.42	up	0.02391
rc_H20989_s_at	H20989	1899	pyruvate kinase, muscle	11.37	up	0.0375
rc_H24077_at	H24077	1900	EST	3.05	up	0.0324
rc_H27188_f_at	H27188	1908	collagen-binding protein 2 (collagen 2)	4.16	up	0.02073
rc_H28333_f_at	H28333	1912	melanoma adhesion molecule	3.11	up	0.00172
rc_H29565_at	H29565	1913	EST	3.89	up	0.01856
rc_H38240_s_at	H38240	1916	thrombospondin 2	4.28	up	0.0066
rc_H38588_s_at	H38588	1918	EST	4.86	up	0.0003
rc_H42321_f_at	H42321	1928	ribosomal protein L18a	3.23	up	0.01102
H43286_s_at	H43286	1929	gamma-aminobutyric acid (GABA) B receptor, 1	5.02	up	0.01972
rc_H43646_at	H43646	1930	H2A histone family, member Y	4.6	up	0.00147
rc_H46486_s_at	H46486	1932	nesca protein	4.77	up	0.00421
rc_H499637_s_at	H499637	1940	EST	3.79	up	0.01092
rc_H52673_s_at	H52673	1943	BCL2-antagonist/killer 1	3.03	up	0.0393
H53657_s_at	H53657	1945	adenylylate cyclase 3	3.98	up	0.0045
H55437_at	H55437	1948	kraken-like	3.53	up	0.02344
rc_H56345_r_at	H56345	1950	EST	4.15	up	0.00488
			solute carrier family 2 (facilitated glucose transporter), member			
rc_H58873_s_at	H58873	1961	1	57.98	up	0.00063
rc_H59617_at	H59617	1964	EST	3.3	up	0.04588
rc_H75933_f_at	H75933	1998	laminin receptor 1 (67kD, ribosomal protein SA)	5.81	up	0.00024
rc_H78211_at	H78211	2001	EST	6.73	up	0.02488
rc_H78323_at	H78323	2002	transcription factor Dp-1	3.69	up	0.00326
			high-mobility group (nonhistone chromosomal) protein isoforms			
rc_H81413_f_at	H81413	2007	I and Y	5.82	up	0.00769
rc_H88674_s_at	H88674	2021	collagen, type I, alpha 2	5.06	up	0.00866
H89551_s_at	H89551	2024	EST	9.94	up	0.00137
rc_H93021_at	H93021	2033	peptidylprolyl isomerase A (cyclophilin A)	3.31	up	0.0183
rc_H93492_at	H93492	2037	EST	3.94	up	0.01136

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_H93652_f_at	H93652	2039	ribosomal protein S5	3.31	up	0.00788
rc_H94471_at	H94471	2042	occludin	43.09	up	0
rc_H95233_s_at	H95233	2048	serine protease inhibitor, Kunitz type, 2	47.06	up	0
rc_H96975_at	H96975	2057	EST	3.22	up	0.0141
rc_H97013_at	H97013	2059	ephrin-A4	9.14	up	0.00346
rc_H97809_at	H97809	2063	EST	4.05	up	0.00111
rc_H98924_at	H98924	2072	chromatin assembly factor 1, subunit A (p150)	3.53	up	0.02106
rc_H89473_s_at	H99473	2077	regulator of nonsense transcripts 1	5.37	up	0.00177

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
J03459_at	J03459	2093	leukotriene A4 hydrolase	3.03	up	0.04041
J03464_s_at	J03464	2094	collagen, type I, alpha 2 solute carrier family 25 (mitochondrial carrier; adenine	9.81	up	0.00028
J03592_at	J03592	2096	nucleotide translocator), member 6	10.05	up	0
J03827_at	J03827	2100	nuclease sensitive element binding protein 1	4.45	up	0.00015
			membrane component, chromosome 1, surface marker 1			
J04152_mna1_s_at	J04152	2107	(40kD glycoprotein, Identified by monoclonal antibody GA733)	5.26	up	0.02466
J04164_at	J04164	2108	Interferon induced transmembrane protein 1 (9-27)	12.37	up	0.00001
AFFX-BioDn-3_at	J04423	2109	EST	54.11	up	0.02774
AFFX-BioDn-3_at	J04423	2109	EST	48.05	up	0.02203
AFFX-BioDn-3_at	J04423	2109	EST	21.46	up	0.04283
AFFX-BioB-3_at	J04423	2109	EST	5.13	up	0.02791
AFFX-BioB-5_at	J04423	2109	EST	4.47	up	0.02754
AFFX-BioDn-3_st	J04423	2109	EST	4.35	up	0.01245
J04469_at	J04469	2111	creatine kinase, mitochondrial 1 (ubiquitous)	7.9	up	0.00705
J04823_mna1_at	J04823	2115	cytochrome c oxidase subunit VIII	3.35	up	0.00075
J05257_at	J05257	2118	dipeptidase 1 (renal)	12.02	up	0.02099
J05582_s_at	J05582	2121	mucin 1, transmembrane solute carrier family 2 (facilitated glucose transporter), member	5.39	up	0.00056
K03195_at	K03195	2128	1	10.73	up	0.00139
K03460_at	K03460	2129	tubulin, alpha 1 (testis specific)	7.5	up	0.00002
L03411_s_at	L03411	2134	RD RNA-binding protein	3.97	up	0.00422
L04483_s_at	L04483	2136	ribosomal protein S21	4.2	up	0.00057
L04490_at	L04490	2137	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD)	5.22	up	0.02192

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
L06499_at	L06499	2141 ribosomal protein L37a	4.34	up	0.01103
L06505_at	L06505	2142 ribosomal protein L12	5	up	0.00163
L08044_s_at	L08044	2149 trefoil factor 3 (intestinal)	21.42	up	0.01674
L08044_s_at	L08044	2149 trefoil factor 3 (intestinal)	14.18	up	0.02124
L09604_at	L09604	2151 proteolipid protein 2 (colonic epithelium-enriched)	8.68	up	0
L11566_at	L11566	2156 ribosomal protein L18	4.29	up	0.00014
L11669_at	L11669	2157 tetracycline transporter-like protein	6.75	up	0.00101
L12350_at	L12350	2160 thrombospondin 2	3.78	up	0.00061
L12711_s_at	L12711	2161 transketolase (Wernicke-Korsakoff syndrome) high-mobility group (nonhistone chromosomal) protein isoforms	3.08	up	0.03362
L17131_m1_at	L17131	2168 I and Y	20.57	up	0.00058
L19527_at	L19527	2169 ribosomal protein L27	3.54	up	0.00025
L19605_at	L19605	2170 annexin A11	6.38	up	0.00017
L19686_m1_at	L19686	2171 macrophage migration inhibitory factor (glycosylation-inhibiting factor)	5.26	up	0.00562
L20591_at	L20591	2173 annexin A3	4.64	up	0.00065
L20941_at	L20941	2174 ferritin, heavy polypeptide 1	3.3	up	0.01172
L21954_at	L21954	2177 benzodiazepine receptor (peripheral)	8.53	up	0.00001
L23808_at	L23808	2179 matrix metalloproteinase 12 (macrophage elastase)	6.18	up	0.02195
L25081_at	L25081	2180 ras homolog gene family, member C	3.67	up	0.00005
L33075_at	L33075	2195 IQ motif containing GTPase activating protein 1	3.83	up	0.00015
L33842_m1_at	L33842	2197 IMP (inosine monophosphate) dehydrogenase 2	11.03	up	0.00001
L33930_s_at	L33930	2198 CD24 antigen (small cell lung carcinoma cluster 4 antigen) transcription elongation factor B (SII), polypeptide 1 (15kD, elongin C)	9.16	up	0.01252
L34587_at	L34587	2200 bixtin-like	4.32	up	0.00287
L36720_at	L36720	2205 RNA-binding protein (autoantigenic)	3.46	up	0.00094
L38696_at	L38696	2208 thyroid receptor interacting protein 10 (CDC42-interacting protein)	3.7	up	0.00093
L40379_at	L40379	2210 peroxisome proliferative activated receptor, gamma	3.87	up	0.00207
L40904_at	L40904	2212	3.43	up	0.03511

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
L41351_at	L41351	2214 protease, serine, 8 (prostasin)	6.34	up	0.01132
L44538_at	L44538	2217 EST	4.34	up	0.04319
L76191_at	L76191	2222 Interleukin-1 receptor-associated kinase 1	5.66	up	0.00089
L76200_at	L76200	2223 guanylate kinase 1	3.24	up	0.0097
AFFX-HUMRGEM1009E M10098	2231	EST	11.55	up	0.00099
AFFX-HUMRGEM1009E M10098	2231	EST	10.2	up	0.00027
AFFX-HUMRGEM1009E M10098	2231	EST	5.62	up	0.00251
AFFX-HUMRGEM1009E M10098	2231	EST	5.61	up	0.01238
AFFX-HUMRGEM1009E M10098	2231	EST	5.35	up	0.00186
AFFX-HUMRGEM1009E M10098	2231	EST	4.79	up	0.00328
AFFX-HUMRGEM1009E M10098	2231	EST	4.66	up	0.00405
AFFX-HUMRGEM1009E M10098	2231	EST	3.73	up	0.01794
M12125_at	M12125	tropomyosin 2 (beta)	10.83	up	0.00191
M13934_cds2_at	M13934	ribosomal protein S14	3.99	up	0
M14199_s_at	M14199	laminin receptor 1 (67kD, ribosomal protein SA)	7.01	up	0
M14483_maf1_s_at	M14483	prothymosin, alpha (gene sequence 28)	4.46	up	0.00686
M14949_at	M14949	related RAS viral (r-ras) oncogene homolog	3.11	up	0.00013
M15205_at	M15205	thymidine kinase 1, soluble	3.75	up	0.00159
M16364_s_at	M16364	creatine kinase, brain	12.69	up	0.03633
M17733_at	M17733	thymosin, beta 4, X chromosome	4.15	up	0.00009
M17885_at	M17885	ribosomal protein, large, P0	3.92	up	0.00003
M17886_at	M17886	ribosomal protein, large, P1	4.34	up	0.00004
M18000_at	M18000	ribosomal protein S17	3.79	up	0.00004
M18728_at	M18728	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	44.82	up	0.00291
M20471_at	M20471	clathrin, light polypeptide (Lca)	5.32	up	0.00344
M22960_at	M22960	protective protein for beta-galactosidase (galactostalidosis)	4.49	up	0.00898
M23613_at	M23613	nucleophosmin (nuclear phosphoprotein B23, numatrin)	3.67	up	0.00977

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
M24194_at	M24194	2302	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	4.55	up	0.00017
M24485_s_at	M24485	2304	glutathione S-transferase pi	10.2	up	0.00003
M26708_s_at	M26708	2311	prothymosin, alpha (gene sequence 28)	3.35	up	0.00064
M27826_at	M27826	2313	endogenous retroviral protease	26.36	up	0.00342
AFFX-M27830_5_at	M27830	2314	EST	15.53	up	0.00022
AFFX-M27830_5_at	M27830	2314	EST	14.86	up	0.00043
AFFX-M27830_5_at	M27830	2314	EST	10.64	up	0.00213
AFFX-M27830_M_at	M27830	2314	EST	9.8	up	0.00041
AFFX-M27830_M_at	M27830	2314	EST	8.78	up	0.00003
AFFX-M27830_5_at	M27830	2314	EST	8.2	up	0.00294
AFFX-M27830_M_at	M27830	2314	EST	6.25	up	0.00046
AFFX-M27830_M_at	M27830	2314	EST	5.78	up	0.0017
M29277_at	M29277	2316	melanoma adhesion molecule	3.91	up	0.00112
M29540_at	M29540	2317	carcinoembryonic antigen-related cell adhesion molecule 5	36.57	up	0.0116
M30496_at	M30496	2324	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thioesterase)	3.8	up	0.00478
M31303_ma1_at	M31303	2327	leukemia-associated phosphoprotein p18 (stathmin)	7.48	up	0.00021
M31520_ma1_s_at	M31520	2328	ribosomal protein S24	3.37	up	0.00077
M31520_at	M31520	2328	ribosomal protein S24	3.13	up	0.00014
M32405_at	M32405	2334	ribosomal protein S15	4.01	up	0.00055
M32886_at	M32886	2335	sorcin	8.35	up	0.00215
AFFX-HUMANGAPDH/M33	M33197	2337	glyceraldehyde-3-phosphate dehydrogenase	3.31	up	0.00009
M34182_at	M34182	2340	protein kinase, cAMP-dependent, catalytic, gamma	4.51	up	0.00043
M35252_at	M35252	2343	transmembrane 4 superfamily member 3	39.12	up	0
M36072_at	M36072	2347	ribosomal protein L7a	3.1	up	0.00006
M38591_at	M38591	2350	S100 calcium-binding protein A10 (annexin I ligand, calpastatin I,	14.87	up	0
M38690_at	M38690	2351	light polypeptide (p11))	9.08	up	0.00059
M55998_s_at	M55998	2356	CD9 antigen (p24)	6.99	up	0.00103
			collagen, type I, alpha 1			

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
M57710_at	M57710	lectin, galactoside-binding, soluble, 3 (galectin 3)	27.12	up	0.00001
M60784_s_at	M60784	small nuclear ribonucleoprotein polypeptide A	5.74	up	0.00126
M60854_at	M60854	ribosomal protein S16	3.4	up	0.00001
M62895_s_at	M62895	annexin A2, annexin A2 pseudogene 2	6.11	up	0.00013
M64716_at	M64716	ribosomal protein S25	3.16	up	0.00039
M68864_at	M68864	ORF	3.1	up	0.00603
M77232_ma1_at	M77232	ribosomal protein S6	3.82	up	0.00045
M77349_at	M77349	transforming growth factor, beta-induced, 68kD	4.81	up	0.00546
M77836_at	M77836	pyrroline-5-carboxylate reductase 1	3.43	up	0.00759
M79463_s_at	M79463	promyelocytic leukemia	4.88	up	0.01821
M81757_at	M81757	ribosomal protein S19	5.46	up	0
M86400_at	M86400	tyrosine 3-monooxygenase/trypophan 5-monooxygenase activation protein, zeta polypeptide	5.62	up	0.00016
M86667_at	M86667	nucleosome assembly protein 1-like 1	3.03	up	0.04853
M86752_at	M86752	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	7.32	up	0.00001
M87339_at	M87339	replication factor C (activator 1) 4 (37kD)	4.07	up	0.00316
M91083_at	M91083	chromosome 11 open reading frame 13	3.3	up	0.00163
M93036_at	M93036	membrane component, chromosomal 4, surface marker (35kD glycoprotein)	16.45	up	0.00308
M94250_at	M94250	midline (neurite growth-promoting factor 2)	10.39	up	0.01818
M94345_at	M94345	capping protein (actin filament), gelsolin-like	22.38	up	0.00003
M96739_at	M96739	nescient helix loop helix 1	3.72	up	0.00015
rc_N20198_s_at	N20198	ubiquitin-conjugating enzyme E2 variant 1	5.17	up	0.00508
rc_N21359_at	N21359	EST	4.43	up	0.00078
rc_N22015_at	N22015	EST	46.61	up	0.00025
rc_N22107_at	N22107	EST	6.88	up	0.04259
rc_N24899_at	N24899	EST	3.06	up	0.00353
rc_N26186_at	N26186	EST	6.15	up	0.00135
rc_N27186_at	N27186	EST	3.79	up	0.00112
rc_N27334_at	N27334	EST	3.65	up	0.03437

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
rc_N29888_at	N29888	2483	EST	3.7	up	0.00226
rc_N30436_f_at	N30436	2484	EST	3.45	up	0.02356
rc_N31570_at	N31570	2486	TNF receptor-associated factor 5	10.39	up	0.00018
rc_N31597_s_at	N31597	2487	DKFZP564G2022 protein	4.44	up	0.00085
N36432_at	N36432	2507	erythrocyte membrane protein band 4.1-like 2	3.03	up	0.03086
rc_N39099_at	N39099	2508	EST	4.42	up	0.00643
rc_N39237_at	N39237	2511	EST	9.29	up	0.00001
rc_N39254_s_at	N39254	2512	EST	4.42	up	0.00478
rc_N46423_at	N46423	2521	EST	9.64	up	0.00027
rc_N47956_at	N47956	2524	eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD)	6.34	up	0.00251
rc_N49284_s_at	N49284	2537	v-myb avian myeloblastosis viral oncogene homolog	11.82	up	0.01981
rc_N49738_at	N49738	2539	EST	3.81	up	0.02479
rc_N50048_at	N50048	2542	EST	4.08	up	0.00085
rc_N51053_s_at	N51053	2543	eukaryotic translation initiation factor 5	3.42	up	0.01326
rc_N51342_at	N51342	2545	EST	3.56	up	0.0001
rc_N52168_at	N52168	2551	EST	5.65	up	0.00003
rc_N54841_at	N54841	2572	EST	42.96	up	0.00002
rc_N56935_s_at	N56935	2575	EST	3.57	up	0.00282
rc_N58463_at	N58463	2580	PCTAIRE protein kinase 1	3.18	up	0.00649
rc_N62126_at	N62126	2589	EST	8.51	up	0.00016
rc_N62675_s_at	N62675	2594	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16	3.61	up	0.04034
rc_N62819_at	N62819	2595	EST	3.25	up	0.01137
rc_N64616_at	N64616	2611	EST	3.11	up	0.0074
rc_N66139_s_at	N66139	2615	neurochondrin homolog of mouse quaking QKI (KH domain RNA binding protein)	4.03	up	0.00118
rc_N66624_at	N66624	2618		6.25	up	0
rc_N66951_at	N66951	2621	EST	5.54	up	0.02442
rc_N67205_at	N67205	2625	EST	3.1	up	0.00626
rc_N68038_f_at	N68038	2632	phorbolin (similar to apolipoprotein B mRNA editing protein)	3.75	up	0.01041

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_N68385_f_at	N68385	2635	ribosomal protein L13a	3.57	up	0.00417
rc_N68921_at	N68921	2639	EST	4.4	up	0.00989
rc_N69252_f_at	N69252	2647	ferritin, light polypeptide	5.33	up	0.01554
rc_N69263_at	N69263	2648	EST	7.47	up	0.00004
rc_N70577_at	N70577	2659	EST	3.07	up	0.01975
rc_N70678_s_at	N70678	2660	TAR (HIV) RNA-binding protein 1	4.2	up	0.00119
rc_N70903_at	N70903	2662	EST	4.41	up	0.00778
rc_N71072_at	N71072	2664	EST	5.57	up	0.03881
rc_N71781_at	N71781	2666	EST	7.01	up	0.02952
rc_N72116_s_at	N72116	2668	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	9.01	up	0.00051
rc_N73762_f_at	N73762	2678	EST	6.65	up	0.0023
rc_N73808_f_at	N73808	2679	EST	8.46	up	0.01886
rc_N73846_at	N73846	2680	EST	3.27	up	0.00012
rc_N77947_s_at	N77947	2698	EST	5	up	0.00117
rc_N80703_at	N80703	2704	EST	6.06	up	0.00003
rc_N89670_at	N89670	2709	EST	4.26	up	0.00002
rc_N89937_at	N89937	2711	LIM domain only 7	3.6	up	0.00375
rc_N90238_i_at	N90238	2712	EST	3.06	up	0.00354
rc_N91023_at	N91023	2716	amyloid beta (A4) precursor protein-binding, family A, member	3.87	up	0.00008
rc_N92775_at	N92775	2723	3 (X11-like 2)	3.86	up	0.00577
rc_N92915_at	N92915	2724	brefeldin A-inhibited guanine nucleotide-exchange protein 1	3.1	up	0.00807
rc_N92934_s_at	N92934	2725	cysteine-rich protein 1 (intestinal)	35.52	up	0.002
rc_N93105_f_at	N93105	2728	EST	3.77	up	0.02195
rc_N93798_at	N93798	2738	protein tyrosine phosphatase type IV A, member 3	4.65	up	0.00118
rc_N98464_s_at	N98464	2744	EST	15.95	up	0.00004
rc_N98758_f_at	N98758	2745	EST	3.87	up	0.0074
N99505_at	N99505	2746	EST	3.6	up	0.04499
rc_R02036_at	R02036	2754	EST	8.01	up	0.01012

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_R06251_f_at	R06251	2764 tumor protein D52-like 2	5.57	up	0.00037
rc_R06254_f_at	R06254	2765 tumor protein D52-like 2	4.64	up	0.00039
rc_R06866_s_at	R06866	2774 EST	5.18	up	0.00187
rc_R06986_f_at	R06986	2776 peptidylprolyl isomerase B (cyclophilin B)	3.01	up	0.04418
rc_R22585_at	R22585	2800 EST	4.8	up	0.0424
rc_R26706_s_at	R26706	2803 EST	3.21	up	0.03858
rc_R26744_at	R26744	2804 midline 1 (Opitz/BBB syndrome)	4.32	up	0.00532
rc_R27432_at	R27432	2808 EST	3.62	up	0.00014
rc_R28636_at	R28636	2809 polypeptide 3	3.78	up	0.00765
rc_R31107_at	R31107	2812 EST	4.12	up	0.00003
rc_R33498_s_at	R33498	2820 EST	41.34	up	0.00001
rc_R36947_s_at	R36947	2825 calcium channel, voltage-dependent, beta 3 subunit	4.11	up	0.00006
rc_r38076_s_at	R38076	2828 EST	4.08	up	0.00374
rc_R38239_at	R38239	2830 EST	7.14	up	0.00249
rc_R38280_at	R38280	2831 BCS1 (yeast homolog)-like	3.68	up	0.0009
rc_R38511_s_at	R38511	2832 protein similar to E.coli yndg and R. capsulatus nifR3	5.19	up	0.00015
rc_R39191_s_at	R39191	2834 KIAA1020 protein	4.69	up	0.00456
rc_R40254_at	R40254	2840 EST	5.82	up	0.00304
rc_R43952_at	R43952	2853 homeo box B5	4.11	up	0.04316
rc_R44479_at	R44479	2855 KIAA0552 gene product	4.14	up	0.0181
rc_R44538_at	R44538	2856 EST	5.73	up	0.01015
rc_J45698_at	R45698	2866 EST	3.01	up	0.04766
rc_R45994_f_at	R45994	2867 EST	7.81	up	0.0018
rc_R48447_at	R48447	2871 EST	7.75	up	0.00049
rc_R48589_at	R48589	2874 EST	4.95	up	0.01346
rc_R49084_s_at	R49084	2879 KIAA0770 protein	3.57	up	0.00447
rc_R49216_at	R49216	2880 EST	3.84	up	0.0004
rc_R49395_s_at	R49395	2881 EST	4.38	up	0.00112
rc_R49476_at	R49476	2883 EST	10.95	up	0.00014
rc_R52161_at	R52161	2893 EST	5.84	up	0.03253

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_R53109_f_at	R53109	2899	dimethylarginine dimethylaminohydroilate 2	3.31	up	0.02389
rc_R53109_r_at	R53109	2899	dimethylarginine dimethylaminohydroilate 2	3.22	up	0.00724
rc_R54614_s_at	R54614	2902	EST	3.24	up	0.00526
rc_R55470_at	R55470	2904	EST	3.59	up	0.00515
rc_R56095_s_at	R56095	2906	EST	8.16	up	0.00023
R56678_at	R56678	2908	EST	3.81	up	0.02242
rc_R56880_at	R56880	2909	EST	6.82	up	0.02559
rc_R58974_at	R58974	2910	EST	4.95	up	0.00498
rc_R59352_s_at	R59352	2915	KIAA0296 gene product	4.19	up	0.00393
rc_R61297_s_at	R61297	2920	eukaryotic translation initiation factor 3, subunit 6 (48kD)	6.42	up	0.00126
R69700_at	R69700	2943	EST	6.71	up	0.0021
rc_R70005_at	R70005	2944	EST	4.61	up	0.00037
rc_R70801_s_at	R70801	2950	EST	6.36	up	0.00563
rc_R71082_s_at	R71082	2951	programmed cell death 5	3.6	up	0.01338
rc_R71395_at	R71395	2952	EST	10.42	up	0.00422
rc_R73565_at	R73565	2959	EST	3.29	up	0.03489
O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)						
rc_R76782_s_at	R76782	2963		5.83	up	0.01126
rc_R77631_at	R77631	2967	EST	3.43	up	0.00006
rc_R79580_at	R79580	2970	EST	6.25	up	0.00593
rc_R87989_at	R87989	2979	centrosome associated protein	3.84	up	0.00008
rc_R91819_at	R91819	2984	EST	8.95	up	0.00009
rc_R92994_s_at	R92994	2990	matrix metalloproteinase 12 (macrophage elastase)	11.05	up	0.00248
rc_R95966_l_at	R95966	2997	EST	11.22	up	0.00682
rc_R96924_s_at	R96924	3001	EST	6.18	up	0.03417
rc_R97759_at	R97759	3006	serum/glucocorticoid regulated kinase	5.99	up	0.00221
S54005_s_at	S54005	3020	thymosin, beta 10	7.03	up	0.00334
S56151_s_at	S56151	3021	milk fat globule-EGF factor 8 protein	4.59	up	0.0091
S69272_s_at	S69272	3028	protease inhibitor 6 (placental thrombin inhibitor)	5.15	up	0.00003

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
S73885_s_at		3032	transcription factor AP-4 (activating enhancer-binding protein 4)	4.18	up	0.00005
S78187_at		3036	cell division cycle 25B	8.07	up	0.00009
S81914_at		3038	immediate early response 3	5.46	up	0.01798
rc_T03313_at		3042	dyskeratosis congenita 1, dyskerin	9.63	up	0.00001
rc_T03438_s_at		3043	EST	0.00032		
rc_T03580_f_at		3046	pyruvate kinase, muscle	8.18	up	
rc_T12599_f_at		3056	ribosomal protein L21	24.91	up	0.0001
rc_T15442_f_at		3057	calpain, large polypeptide L1	3.54	up	0.01437
rc_T15473_at		3058	muscle specific gene	5.01	up	0.00255
rc_T15477_at		3059	EST	5.81	up	0.02404
rc_T15903_s_at		3063	EST	3.61	up	0.00005
rc_T16308_f_at		3069	EST	3.23	up	0.01377
				5.29	up	0.00119
rc_T16983_s_at		3074	cleavage and polyadenylation specific factor 4, 30kD subunit	5.23	up	0.00075
rc_T23465_at		3081	EST	4.4	up	0.017
rc_T23490_l_at		3082	EST	11.88	up	0.03242
rc_T23516_f_at		3083	3-phosphoglycerate dehydrogenase	5.38	up	0.00001
rc_T24068_s_at		3088	EST	15.26	up	0.00046
rc_T25725_at		3091	EST	3.26	up	0.00099
rc_T26366_f_at		3093	EST	30.43	up	0.00153
rc_T26471_at		3094	EST	4.62	up	0.01091
rc_T26513_l_at		3095	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	5.07	up	0.0016
rc_T26574_s_at		3096	catenin (cadherin-associated protein), delta 1	3.17	up	0.00828
rc_T30193_s_at		3098	protease, serine, 8 (prostasin)	8.39	up	0.00043
rc_T32072_s_at		3102	EST	5.95	up	0.00029
rc_T32108_at		3103	EST	6.96	up	0.00723
rc_T33489_s_at		3105	EST	8.04	up	0.00469
rc_T33508_s_at		3106	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	3.31	up	0.00416

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	P value
T35341_s_at	T35341	3112 EST	4.73	up	0.00057
T35725_s_at	T35725	3113 EST	3.4	up	0.00149
rc_T40849_s_at	T40849	3116 maternal G10 transcript	4.11	up	0.00449
rc_T47032_s_at	T47032	3124 partner of RAC1 (arfaptin 2)	3.27	up	0.00503
rc_T47325_s_at	T47325	3125 EST	5.63	up	0.01015
rc_T47601_at	T47601	3126 ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	4.05	up	0.00878
rc_T47969_s_at	T47969	3128 eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD)	3.03	up	0.03452
T48195_s_at	T48195	3131 EST	3.75	up	0.00012
rc_T48293_f_at	T48293	3133 EST	3.55	up	0.01355
rc_T53404_at	T53404	3143 EST	10.68	up	0.00582
rc_T55004_s_at	T55004	3146 EST	4.83	up	0.01156
rc_T55196_at	T55196	3147 EST	4.04	up	0.00012
rc_T58153_s_at	T58153	3154 heat shock 105kD	3.08	up	0.01317
rc_T58607_at	T58607	3155 EST	3.52	up	0.04102
rc_T59161_s_at	T59161	3159 thymosin, beta 10	3.41	up	0.01885
rc_T59668_s_at	T59668	3160 lysyl oxidase	3.28	up	0.00588
rc_T66935_at	T66935	3179 EST	3.97	up	0.00188
rc_T77733_s_at	T77733	3219 tubulin, gamma 1	4.42	up	0.00049
rc_T78922_s_at	T78922	3222 stem cell growth factor; lymphocyte secreted C-type lectin	3.42	up	0.02419
rc_T91116_at	T91116	3252 EST	4.01	up	0.02721
rc_T92935_at	T92935	3255 EST	3.48	up	0.03578
rc_T95057_f_at	T95057	3259 EST	10.39	up	0.00003
rc_T98284_at	T98284	3268 EST	4.47	up	0.00054
U01062_at	U01062	3273 Inositol 1,4,5-triphosphate receptor, type 3	7.41	up	0
U01147_at	U01147	3275 active BCR-related gene	3.22	up	0.00103
U02493_at	U02493	3279 non-Pou domain-containing octamer (ATGCCAAAT) binding protein	3.04	up	0.0019

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
U03891_at	U03891	3283	phorbolin (similar to apolipoprotein B mRNA editing protein)	3	up	0.00065
U04313_at	U04313	3284	protease inhibitor 5 (maspin)	4.54	up	0.02986
U05875_at	U05875	3286	interferon gamma receptor 2 (interferon gamma transducer 1)	3.09	up	0.00549
U07969_s_at	U07969	3289	cadherin 17, L1 cadherin (liver-intestine)	10.78	up	0.02002
U09117_at	U09117	3294	phospholipase C, delta 1	7.96	up	0.00001
U09564_at	U09564	3295	SFRS protein kinase 1	3.79	up	0.00765
U09770_at	U09770	3296	cysteine-rich protein 1 (intestinal)	13.03	up	0.0072
U11861_at	U11861	3298	maternal G10 transcript	3.8	up	0.00001
U12404_at	U12404	3299	ribosomal protein L10a	4.18	up	0.00004
U12465_at	U12465	3300	ribosomal protein L35	4.69	up	0.00001
U14968_at	U14968	3303	ribosomal protein L27a	4.01	up	0.00003
U14969_at	U14969	3304	ribosomal protein L28	4.63	up	0.00004
U14970_at	U14970	3305	ribosomal protein S5	3.45	up	0.00915
U14971_at	U14971	3306	ribosomal protein S9	3.93	up	0.00026
U14972_at	U14972	3307	ribosomal protein S10	5.24	up	0.00077
U14973_at	U14973	3308	ribosomal protein S29	3.1	up	0.00028
U15008_at	U15008	3309	small nuclear ribonucleoprotein D2 polypeptide (16.5kD)	4.9	up	0.00396
U17077_at	U17077	3314	BENF protein	4.98	up	0.00366
U17760_ma1_at	U17760	3315	laminin, beta 3 (nlicein (125kD), kallinin (140kD), BM600 (125kD))	3.54	up	0.01853
U20499_at	U20499	3321	sulfotransferase family 1A, phenol-preferring, member 3	5.5	up	0.00299
U20758_ma1_at	U20758	3323	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	6.12	up	0.03448
U21049_at	U21049	3325	epithelial protein up-regulated in carcinoma, membrane	7.53	up	0.01667
U22376_cds2_s_at	U22376	3328	associated protein 17	3.34	up	0.03416
U25789_at	U25789	3334	v-myb avian myeloblastosis viral oncogene homolog	4.37	up	0.00045

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
				3.45	up	0.02342
U26726_at	U26726	3336	hydroxysteroid (11-beta) dehydrogenase 2	3.45	up	0.02342
U27328_s_at	U27328	3338	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included)	3.05	up	0.03224
U31556_at	U31556	3346	E2F transcription factor 5, p130-binding	4.14	up	0.01157
U33286_at	U33286	3349	chromosome segregation 1 (yeast homolog)-like	3.39	up	0.00939
U36241_ma1_at	U36241	3351	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	3.05	up	0.02622
U37689_at	U37689	3356	polymerase (RNA) II (DNA directed) polypeptide H	3.65	up	0.00044
U40990_at	U40990	3359	potassium voltage-gated channel, KQT-like subfamily, member 1	3.18	up	0.00093
U42408_at	U42408	3361	ladinin 1	6.8	up	0.00305
U43901_ma1_s_at	U43901	3362	laminin receptor 1 (67kD, ribosomal protein SA)	3.11	up	0.03145
U46692_ma1_at	U46692	3367	cystatin B (stefin B)	5.54	up	0.00016
U47025_s_at	U47025	3368	phosphorylase, glycogen; brain	8.52	up	0.00134
U48705_ma1_s_at	U48705	3370	discoidin domain receptor family, member 1	5.94	up	0.01323
U51095_at	U51095	3382	caudal type homeo box transcription factor 1	4.76	up	0.02664
U51478_at	U51478	3385	ATPase, Na+/K+ transporting, beta 3 polypeptide	5.75	up	0.00007
			solute carrier family 1 (neutral amino acid transporter), member			
U53347_at	U53347	3389	3	3.81	up	0.00273
U53830_at	U53830	3391	Interferon regulatory factor 7	3.94	up	0.03147
U58682_at	U58682	3396	ribosomal protein S28	6.09	up	0.00001
U62392_at	U62392	3403	zinc finger protein 193	3.18	up	0.00269
U62962_at	U62962	3404	eukaryotic translation initiation factor 3, subunit 6 (48kD)	4.05	up	0.0047
U67171_at	U67171	3409	selenoprotein W, 1	3.08	up	0.0047
U73379_at	U73379	3418	ubiquitin carrier protein E2-C	8.32	up	0.00101
U73843_at	U73843	3421	E74-like factor 3 (ets domain transcription factor)	5.75	up	0.00017
U75285_ma1_at	U75285	3422	apoptosis inhibitor 4 (survivin)	4.46	up	0.02212
U76366_s_at	U76366	3424	Treacher Collins-Franceschetti syndrome 1	3.44	up	0.00021
U78027_ma3_at	U78027	3429	EST	4.15	up	0.00295
U78095_at	U78095	3430	serine protease inhibitor, Kunitz type, 2	18.85	up	0

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
U78525_at	U78525	3432	eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)	4.68	up	0.00132
U78558_at	U78556	3433	cisplatin resistance associated	5.77	up	0.00241
U79266_at	U79266	3434	protein predicted by clone 23627	3.49	up	0.00004
U79725_at	U79725	3438	glycoprotein A33 (transmembrane)	8.57	up	0.00299
U83246_at	U83246	3443	copine 1	3.57	up	0.01672
U84720_at	U84720	3446	RAE1 (RNA export 1, S.pombe) homolog	3.37	up	0.03586
U85773_at	U85773	3449	phosphomannomutase 2	3.94	up	0.00288
U86409_at	U86409	3450	EST	3.38	up	0.00003
U89606_at	U89606	3452	pyridoxal (pyridoxine, vitamin B6) kinase	3.58	up	0.00322
U90549_at	U90549	3456	high-mobility group (nonhistone chromosomal) protein 17-like 3	3.2	up	0.0401
U90913_at	U90913	3459	Tax interaction protein 1	4.35	up	0.00159
U93205_at	U93205	3461	chloride intracellular channel 1	6.14	up	0.00058
U93868_at	U93868	3463	polymerase (RNA) III (DNA directed) (32kD)	3.5	up	0.01235
rc_W02041_at	W02041	3466	EST	4.83	up	0.00158
rc_W20391_s_at	W20391	3479	kinuin-like 2	3.98	up	0.01788
W28362_at	W28362	3488	KIAA0974 protein	3.98	up	0.00626
rc_W31382_at	W31382	3495	EST	4	up	0.00058
rc_W37680_at	W37680	3503	EST	3.55	up	0.01036
rc_W37937_at	W37937		EST	3.07	up	0.00776
rc_W38044_s_at	W38044		myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 7	7.28	up	0.03105
W39183_s_at	W39183	3508	KIAA0601 protein	3.66	up	0.00018
rc_W42827_f_at	W42827	3511	EST	3.56	up	0.00198
rc_W42957_at	W42957	3516	calmodulin 2 (phosphorylase kinase, delta)	15.22	up	0.00007
rc_W44557_at	W44557	3518	chromosome 1 open reading frame 2	4.32	up	0.00128
rc_W44733_at	W44733	3519	EST	3.02	up	0.00097
rc_W45487_s_at	W45487	3524	dynamin 2	4.2	up	0.00325
rc_W49574_at	W49574	3538	EST	5.97	up	0.00045
rc_W49661_s_at	W49661	3539	FK506-binding protein 9 (63 kD)	3.01	up	0.02259

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
W52858_at	W52858	3545	DKFZP564F0522 protein	4.38	up	0.00088
rc_W60486_at	W60486	3558	EST	4.29	up	0.00964
rc_W67251_s_at	W67251	3570	EST	6.13	up	0.01463
rc_W70336_at	W70336	3579	EST	3.65	up	0.01776
rc_W72276_at	W72276	3583	EST	27.39	up	0.00183
rc_W72861_at	W72861	3586	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	3.01	up	0.00055
rc_W73189_at	W73189	3589	EphB2	3.69	up	0.02098
rc_W73914_at	W73914	3595	EST	3.5	up	0.04782
rc_W74233_s_at	W74233	3597	related RAS viral (r-ras) oncogene homolog	6.02	up	0.01815
W76097_at	W76097	3599	EST	0.00001		
rc_W78057_at	W78057	3600	EST	3.83	up	0.00001
rc_W80730_at	W80730	3607	EST	9.06	up	0.0034
rc_W80763_at	W80763	3608	EST	6.59	up	0.00425
rc_W81375_at	W81375	3613	EST	3.83	up	0.01319
rc_W81540_at	W81540	3614	serine/threonine kinase 24 (Ste20, yeast homolog)	3.58	up	0.00322
rc_W90146_at	W90146	3644	EST	6.72	up	0.00164
rc_W92207_at	W92207	3651	EST	6.23	up	0.01558
rc_W92207_f_at	W922449	3652	EST	6.77	up	0.00002
rc_W92608_s_at	W92608	3653	BAL1-associated protein 3	31.67	up	0.00011
rc_W93726_s_at	W93726	3656	protease inhibitor 5 (maspin)	5.12	up	0.00075
rc_W93943_at	W93943	3657	EST	16.48	up	0.00014
W95348_at	W95348	3663	HSPC113 protein	4.3	up	0.00296
rc_W95477_at	W95477	3664	EST	10.89	up	0.01065
X03342_at	X03342	3675	ribosomal protein L32	26.51	up	0.00161
AFFX-CreX-5_at	X03453	3677	EST	4.09	up	0.00008
X04347_s_at	X04347	3680	heterogeneous nuclear ribonucleoprotein A1	3.03	up	0.00025
X05610_at	X05610	3685	collagen, type IV, alpha 2	7.26	up	0.00018
X06617_at	X06617	3687	ribosomal protein S11	3.58	up	0.01351
X07820_at	X07820	3695	matrix metalloproteinase 10 (stromelysin 2)	4.32	up	0.0002
				3.49	up	0.00689

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	P value
X12447_at	X12447	3696 aldolase A, fructose-bisphosphate	10.52	up	0.00038
X13956_at	X13956	3701 EST	3.2	up	0.00321
X14850_at	X14850	3706 H2A histone family, member X	4.11	up	0.0001
X15940_at	X15940	3709 ribosomal protein L31	4.45	up	0.00004
X17093_at	X17093	3716 EST	4.82	up	0.00176
X17206_at	X17206	3718 ribosomal protein S2	5.14	up	0
X17567_s_at	X17567	3719 small nuclear ribonucleoprotein polypeptides B and B1	3.6	up	0.00586
X51466_at	X51466	3720 eukaryotic translation elongation factor 2	3.25	up	0.00019
X51521_at	X51521	3721 villin 2 (ezrin)	3.89	up	0.00001
X52851_rna1_at	X52851	3725 EST	3.38	up	0.0001
X52966_at	X52966	3726 ribosomal protein L35a	3.93	up	0.00217
X53331_at	X53331	3727 matrix Gla protein	3.66	up	0.04038
X54667_s_at	X54667	3731 cystatin S, cystatin SN	8.53	up	0.00059
X55715_at	X55715	3735 ribosomal protein S3	3.72	up	0.00755
X55954_at	X55954	3736 ribosomal protein L23	3.81	up	0.00025
X56494_at	X56494	3738 pyruvate kinase, muscle	22.97	up	0.00001
X56932_at	X56932	3740 ribosomal protein L13a	3.26	up	0
X56997_rna1_at	X56997	3741 ubiquitin A-52 residue ribosomal protein fusion product 1	3.18	up	0.00006
X57348_s_at	X57348	3744 stratin	12.53	up	0.0013
X62535_at	X62535	3756 diacylglycerol kinase, alpha (80kD)	4.72	up	0.00315
X62691_at	X62691	3757 ribosomal protein S15a	4.09	up	0.00005
X63527_at	X63527	3761 ribosomal protein L19	3.17	up	0.02488
X63629_at	X63629	3762 cadherin 3, P-cadherin (placental)	3.02	up	0.01654
X64364_at	X64364	3764 basigin	6.45	up	0.00041
X64707_at	X64707	3765 ribosomal protein L13	4.28	up	0.00257
X65614_at	X65614	3767 S100 calcium-binding protein P	12.2	up	0.00065
X66364_at	X66364	3770 cyclin-dependent kinase 5	3.55	up	0.02824
X66401_cds1_at	X66401	3771 proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)	3.68	up	0.01385
X66899_at	X66899	3772 Ewing sarcoma breakpoint region 1	4.72	up	0.00011

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
X67247_mna1_at	X67247	3774 mitogen-activated protein kinase kinase kinase 3	3.48	up	0.00012
X67325_at	X67325	3775 interferon, alpha-inducible protein 27	9.67	up	0.03245
X68314_at	X68314	3778 glutathione peroxidase 2 (gastrointestinal)	14.4	up	0.00222
X68688_mna1_s_at	X68688	3780 zinc finger protein 33a (KOX 31)	4.7	up	0.00062
X68688_mna1_s_at	X68688	3780 zinc finger protein 33a (KOX 31)	3.62	up	0.00319
X69150_at	X69150	3782 ribosomal protein S18	4.5	up	0.00003
X69391_at	X69391	3783 ribosomal protein L6	3.18	up	0.00003
X69398_at	X69398	3784 CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	3.68	up	0.02332
X69654_at	X69654	3785 ribosomal protein S26	3.11	up	0.02683
X69908_mna1_at	X69908	3786 ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	3.73	up	0.00685
X70040_at	X70040	3788 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	4	up	0.00402
X74929_s_at	X74929	3792 keratin 8	4.73	up	0.00018
X76180_at	X76180	3795 sodium channel, nonvoltage-gated 1 alpha	11.68	up	0
X77588_s_at	X77588	3799 N-acetyltransferase, homolog of <i>S. cerevisiae</i> ARD1	3.91	up	0.0221
X78687_at	X78687	3800 sialidase 1 (lysosomal sialidase)	3.18	up	0.031
X79234_at	X79234	3803 ribosomal protein L11	3.59	up	0.00051
X79882_at	X79882	3805 lung resistance-related protein	6.71	up	0.0362
X80198_at	X80198	3807 steroidogenic acute regulatory protein related	3.03	up	0.00044
X80822_at	X80822	3808 ribosomal protein L18a	4.13	up	0.0006
X80822_f_at	X80822	3808 ribosomal protein L18a	3.08	up	0.02481
X80909_at	X80909	3809 nascent-peptide-associated complex alpha polypeptide	3.84	up	0.00399
X83228_at	X83228	3810 cadherin 17, L1 cadherin (liver-intestine)	10.58	up	0.02147
X89960_at	X89960	3818 EST	9.87	up	0
X92518_s_at	X92518	3825 C high-mobility group (nonhistone chromosomal) protein isoform I-	3.12	up	0.00638
X93036_at	X93036	3830 FXYD domain-containing ion transport regulator 3	42.36	up	0.00167

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
X95404_at	X95404	cofilin 1 (non-muscle)	3.18	up	0.00104
X98482_f_at	X98482	EST	5.03	up	0.00002
X99133_at	X99133	lipocalin 2 (oncogene 24p3)	6.27	up	0.0453
Y00503_at	Y00503	keratin 19	14.19	up	0.00217
Y00705_at	Y00705	serine protease inhibitor, Kazal type 1	9.83	up	0.03697
Y10807_s_at	Y10807	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2	4.28	up	0.00124
Z23090_at	Z23090	heat shock 27kD protein 1	7.67	up	0.00008
Z24727_at	Z24727	tropomyosin 1 (alpha)	4.47	up	0.00121
Z25749_ma1_at	Z25749	nuclear factor of kappa light polypeptide gene enhancer in B-	4.41	up	0.00031
Z26876_at	Z26876	cells inhibitor-like 2	4.43	up	0.00022
Z28407_at	Z28407	ribosomal protein L38	6.53	up	0.00004
Z30643_at	Z30643	ribosomal protein L8	3.86	up	0.00204
rc_Z38150_s_at	Z38150	chloride channel Ka	3.06	up	0.00049
rc_Z38266_at	Z38266	EST	6.58	up	0.01809
rc_Z38729_at	Z38729	EST	3.13	up	0.04514
rc_Z38909_at	Z38909	EST	3.55	up	0.03195
rc_Z39079_at	Z39079	KIAA1058 protein	4.08	up	0.01781
rc_Z39191_at	Z39191	EST	8.84	up	0.00011
rc_Z39200_at	Z39200	EST	3.29	up	0.05586
rc_Z39429_at	Z39429	EST	7.84	up	0.00045
rc_Z39930_f_at	Z39930	EST	3.07	up	0.00002
rc_Z40583_f_at	Z40583	EST	4.24	up	0.02375
rc_Z40898_at	Z40898	EST	3.71	up	0.01168
rc_Z40945_at	Z40945	trinucleotide repeat containing 15	7.82	up	0.00007
rc_Z41103_at	Z41103	trinucleotide repeat containing 15	3.83	up	0.00444
rc_Z41740_s_at	Z41740	EST	6.76	up	0.00049
rc_Z41798_s_at	Z41798	EST	6	up	0.00073
Z68228_s_at	Z68228	junction plakoglobin	3.3	up	0.0237
Z74615_at	Z74615	collagen, type I, alpha 1	10.47	up	0.00064
Z74616_s_at	Z74616	collagen, type I, alpha 2	4.83	up	0.02364

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA001603_at	AA001603	3 EST	4.31	down	0.00883
rc_AA001604_at	AA001604	4 EST	3.33	down	0.0215
AA004231_at	AA004231	7 EST	3.16	down	0.03067
rc_AA004521_at	AA004521	8 prostate cancer overexpressed gene 1	8.03	down	0.00027
rc_AA004905_at	AA004905	11 KIAA0937 protein	4.63	down	0.00082
rc_AA005202_at	AA005202	12 retinol-binding protein 4, interstitial	3.18	down	0.00106
rc_AA005358_at	AA005358	14 EST	5.2	down	0.00318
rc_AA007629_at	AA007629	19 EST	8.01	down	0.00001
rc_AA009719_at	AA009719	20 peroxisomal membrane protein 2 (22kD)	47.12	down	0.00008
rc_AA010205_at	AA010205	23 EST	7.41	down	0
rc_AA010360_at	AA010360	24 EST	6.55	down	0.00027
rc_AA010530_at	AA010530	25 EST	3.74	down	0.0481
rc_AA010619_at	AA010619	27 EST	8.55	down	0.00057
AA010750_at	AA010750	28 calmodulin 1 (phosphorylase kinase, delta)	10.22	down	0.00959
rc_AA015768_at	AA015768	34 EST	15.3	down	0.00008
rc_AA017146_at	AA017146	36 EST	10.1	down	0.00052
rc_AA017192_at	AA017192	37 EST	3.43	down	0.04865
rc_AA018867_at	AA018867	39 EST	42.87	down	0.00002
rc_AA021623_s_at	AA021623	43 insulin induced gene 1	11.71	down	0.00094
rc_AA025930_at	AA025930	52 EST	3.59	down	0.00372
rc_AA031543_s_at	AA031543	68 translocation protein 1	5.92	down	0.00405
AA031548_at	AA031548	69 cell division cycle 42 (GTP-binding protein, 25kD)	3.65	down	0.03029
AA032005	AA032005	71 EST	5.3	down	0.01202
AA032048	AA032048	72 EST	5.45	down	0.00383
rc_AA032250_at	AA032250	73 EST	3.56	down	0.0009
rc_AA034030_at	AA034030	75 methylmalonyl Coenzyme A mutase	14.32	down	0.00004
rc_AA035245_s_at	AA035245	79 aldehyde oxidase 1	69.82	down	0.00117
rc_AA035457_at	AA035457	80 EST	10.06	down	0.00085
rc_AA035638_at	AA035638	82 EST	9.91	down	0.00541
rc_AA036662_s_at	AA036662	83 EST	4.16	down	0.00235
rc_AA037357_f_at	AA037357	85 EST	3.53	down	0.02129

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA039335_s_at	AA039335	89	coagulation factor XII (Hageman factor)	32	down	0.0029
rc_AA039616_at	AA039616	90	EST	9.36	down	0.00009
AA039806_at	AA039806	91	msh (Drosophila) homeo box homolog 1	3.53	down	0.00114
rc_AA040087_at	AA040087	92	EST	4.13	down	0.00123
rc_AA040270_at	AA040270	93	EST	3.03	down	0.01367
rc_AA040291_at	AA040291	94	KIAA0669 gene product	3.55	down	0.00308
AA043501_at	AA043501	98	v-maf musculoaponeurotic fibrosarcoma (avian)	3.81	down	0.01304
AA044622_at	AA044622	103	EST	3.62	down	0.03789
AA044755_s_at	AA044755	104	EST	6.7	down	0.01228
AA044842_at	AA044842	105	Autosomal Highly Conserved Protein	5.21	down	0.0009
AA045870_at	AA045870	108	EST	5.93	down	0.00017
rc_AA046457_at	AA046457	111	EST	3.2	down	0.00513
AA046674_at	AA046674	112	EST	5.17	down	0.02561
rc_AA046747_at	AA046747	114	EST	4.82	down	0.00022
AA046840_at	AA046840	115	CCAAT/enhancer binding protein (C/EBP), delta	3.79	down	0.03319
AA047151_at	AA047151	116	EST	7.13	down	0.00007
rc_AA047187_at	AA047187	117	EST	3.04	down	0.04306
rc_AA047290_at	AA047290	118	EST	3.39	down	0.00024
rc_AA052980_at	AA052980	122	EST	4.52	down	0.023
rc_AA055992_at	AA055992	136	calumenin	3.51	down	0.00604
AA056170_at	AA056170	137	EST	3.82	down	0.0083
rc_AA056247_at	AA056247	138	EST	3.48	down	0.03277
rc_AA056482_at	AA056482	141	EST	4.82	down	0.00199
rc_AA057678_at	AA057678	143	EST	6.88	down	0.00078
AA059489_at	AA059489	145	RGC32 protein	3.74	down	0.00734
rc_AA062744_at	AA062744	147	EST	3.31	down	0.01909
rc_AA065173_at	AA065173	148	EST	4.08	down	0.00377
rc_AA069456_at	AA069456	149	KIAA0438 gene product	3.47	down	0.02718
rc_AA069768_s_at	AA069768	151	hevin	4.62	down	0.00202
AA070090_at	AA070090	152	EST	3.24	down	0.00804
rc_AA070091_at	AA070091	153	EST	5	down	0

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA074885_at	AA074885	161 macrophage receptor with collagenous structure	11.05	down	0.00786
rc_AA074891_at	AA074891	162 EST	3.12	down	0.01897
rc_AA076238_at	AA076238	168 EST	3.23	down	0.00395
rc_AA076249_at	AA076249	169 EST	3.78	down	0.00029
rc_AA076326_at	AA076326	170 SEC14 (S. cerevisiae)-like 2 solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	10.88	down	0.00616
rc_AA079758_f_at	AA079758	174 Dkfp566f123 protein	7.83	down	0.00359
rc_AA083812_at	AA083812	175 Dkfzp566f123 protein	9.11	down	0.00167
rc_AA084408_at	AA084408	179 EST	4.05	down	0.00864
rc_aa084688_at	AA084688	180 ubiquitin-like 3	3.19	down	0.0419
rc_AA085987_s_at	AA085987	183 UDP glycosyltransferase 1	40.87	down	0.00004
rc_AA086201_at	AA086201	185 EST	5.8	down	0.00012
rc_AA088698_at	AA088698	188 EST	3.23	down	0.02543
AA090257_at	AA090257	190 superoxide dismutase 2, mitochondrial	11.72	down	0.02072
AA090434_at	AA090434	191 diaphanous (Drosophila, homolog) 1	4.61	down	0.01704
AA090439_at	AA090439	192 ribosomal protein S6	5.58	down	0.00501
AA092596_at	AA092596	197 bone morphogenetic protein 6	3.46	down	0.02532
AA092716_at	AA092716	198 HLA-B associated transcript-3	13.97	down	0.00009
AA093923_at	AA093923	200 EST	3.82	down	0.03924
AA094507_s_at	AA094507	201 EST	3.52	down	0.04783
AA094999_at	AA094999	204 zinc finger protein 216	5.12	down	0.0257
rc_AA099225_at	AA099225	206 EST	7.33	down	0.00062
AA099391_s_at	AA099391	207 myosin, light polypeptide kinase	9.07	down	0.00003
rc_AA099589_s_at	AA099589	210 GDP dissociation inhibitor 2	3.7	down	0.04069
rc_AA101055_s_at	AA101055	213 leptin receptor	3.14	down	0.0071
rc_AA101235_at	AA101235	214 EST	8.46	down	0.00822
rc_AA101632_at	AA101632	217 EST	4.19	down	0.00023
rc_AA112101_f_at	AA112101	222 EST	8.5	down	0.00004
rc_AA112209_s_at	AA112209	223 acyl-Coenzyme A dehydrogenase, long chain UDP-N-acetylglucosamine pyrophosphorylase 1;	3.37	down	0.00084
AA114949_at	AA114949	228 Spam associated antigen 2	5.12	down	0.01028

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA121140_at	AA121140	EST	3.33	down	0.00058
rc_AA122345_f_at	AA122345	238 glutamate dehydrogenase 1	16.53	down	0.00004
rc_AA125831_r_at	AA125831	241 myosin, light polypeptide kinase	8.18	down	0.00039
rc_AA125856_at	AA125856	242 EST	3.17	down	0.01545
rc_AA125861_at	AA125861	243 EST	3.69	down	0.01547
rc_AA126059_at	AA126059	246 EST	3.08	down	0.00706
rc_AA126722_s_at	AA126722	251 O-6-methylguanine-DNA methyltransferase	8.26	down	0.002
rc_AA127444_at	AA127444	252 EST	3.56	down	0.0291
rc_AA127514_at	AA127514	253 EST	3.4	down	0.00045
rc_AA133215_at	AA133215	277 calcitonin receptor-like receptor activity modifying	4.55	down	0.02092
rc_AA133296_at	AA133296	278 EST	4.23	down	0.00041
rc_AA133439_at	AA133439	279 EST	4.07	down	0.00022
rc_AA134549_at	AA134549	288 EST	3.36	down	0.03438
rc_AA135558_s_at	AA135558	293 peptidase D	4.17	down	0.00668
rc_AA135958_at	AA135958	296 EST	4.02	down	0.00012
rc_AA136079_at	AA136079	297 EST	4.26	down	0.0057
rc_AA142849_at	AA142849	306 EST	7.59	down	0.00804
AA143019_at	AA143019	309 EST	6.75	down	0.00109
rc_aa147646_s_at	AA147646	317 DKFZP586A0522 protein	21.82	down	0
rc_AA148480_s_at	AA148480	318 flavin containing monooxygenase 5	19.64	down	0
rc_AA148923_at	AA148923	321 decidual protein induced by progesterone	13.2	down	0.00257
rc_AA149253_at	AA149253	323 EST	5.12	down	0.00863
rc_AA150776_at	AA150776	330 EST	10.45	down	0.00015
rc_AA150891_at	AA150891	331 EST	4.22	down	0.01692
rc_AA151210_at	AA151210	333 EST	4.61	down	0.00008
rc_AA151676_at	AA151676	337 peptidyl arginine deiminase, type II	4.01	down	0.00911
rc_AA156336_at	AA156336	341 nuclear receptor co-repressor 1	3.69	down	0.01276
rc_AA156565_at	AA156565	344 neuronal SNAP25-like 1	15.01	down	0.01387
rc_AA157112_at	AA157112	345 EST	3.94	down	0.02571
AA157520_at	AA157520	347 EST	3.18	down	0.00516

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA157799_at	AA157799	348	aldo-keto reductase family 7, member A2 (afatoxin aldehyde reductase)	5.96	down	0
rc_AA164588_s_at	AA164586	359	estrogen receptor 1	5.8	down	0.00182
rc_AA167565_at	AA167565	362	EST	8.08	down	0.00046
rc_AA171694_at	AA171694	366	ceruloplasmin (ferroxidase)	21.23	down	0.00179
rc_AA172372_at	AA172372	370	EST	6.48	down	0.00344
rc_AA176233_at	AA176233	376	EST	11.44	down	0.01856
rc_AA179004_at	AA179004	377	EST	14.34	down	0.00008
rc_AA179387_at	AA179387	379	DKFZP434N126 protein	3.7	down	0.01588
rc_AA180356_at	AA180356	382	EST	3.16	down	0.00917
rc_AA182030_at	AA182030	387	EST	8.32	down	0.00018
rc_AA182568_at	AA182568	388	STAT Induced STAT inhibitor-2	10.92	down	0.00099
AA188921_at	AA188921	393	similar to Caenorhabditis elegans protein	4.05	down	0.004
AA190816_at	AA190816	395	EST	4.1	down	0.00037
AA191014_at	AA191014	396	EST	5.07	down	0.01455
rc_AA191310_s_at	AA191310	397	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR65), beta isoform	7.28	down	0
rc_AA191488_s_at	AA191488	398	solute carrier family 31 (copper transporters),	3.19	down	0.00013
rc_AA191647_at	AA191647	399	ceruloplasmin (ferroxidase)	4.05	down	0.00029
rc_AA193204_at	AA193204	402	Arg/Abl-interacting protein ArgBP2	8.98	down	0.00861
rc_AA193223_at	AA193223	403	EST	4.2	down	0.02416
AA193297_at	AA193297	404	EST	4.37	down	0.04676
rc_AA194075_f_at	AA194075	406	nuclear receptor coactivator 4	4.69	down	0.00862
AA194146_at	AA194146	407	EST	3.53	down	0.00352
rc_AA194833_at	AA194833	411	claudin 1	11.45	down	0.00034
rc_AA194997_s_at	AA194997	412	EST	16.12	down	0.00103
rc_AA195656_at	AA195656	418	KIAA0977 protein	15.29	down	0.00817
rc_AA195657_at	AA195657	419	EST	6.44	down	0.00016
rc_AA196287_at	AA196287	420	EST	15.07	down	0.00001
rc_AA197311_s_at	AA197311	422	Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	6.07	down	0.00053

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
		AA203222	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	4.21	down	0.00745
rc_AA205724_at	AA205724	424		6.73	down	0.00027
rc_AA207123_at	AA207123	426	EST	3.16	down	0.00328
rc_AA210850_at	AA210850	430	immunoglobulin superfamily, member 3	4.97	down	0.00735
rc_AA211388_at	AA211388	431	EST	4.56	down	0.02703
rc_AA214542_at	AA214542	433	EST	4.43	down	0.00601
rc_AA215585_s_at	AA215585	438	EST	3	down	0.03027
rc_AA215919_at	AA215919	443	nudix (nucleoside diphosphate linked moiety X)-F-box protein 7	6.62	down	0.00921
rc_AA218727_at	AA218727	445	EST	3.47	down	0.00125
rc_AA219039_at	AA219039	446	EST	5.76	down	0.00053
rc_AA219304_s_at	AA219304	447	alpha-2-macroglobulin	21.97	down	0.00011
rc_AA219653_at	AA219653	448	EST	4.08	down	0.00607
rc_AA223335_s_at	AA223335	449	proplyon Coenzyme A carboxylase, beta	5.49	down	0.02761
rc_AA223902_at	AA223902	450	EST	9.91	down	0.00003
rc_AA227452_at	AA227452	455	EST	4.7	down	0.02345
rc_AA227480_s_at	AA227480	456	pim-2 oncogene	3.31	down	0.02413
rc_AA227901_at	AA227901	459	SEC24 (S. cerevisiae) related gene family,	3.18	down	0.00397
rc_AA228119_at	AA228119	462	pre-B-cell colony-enhancing factor	4.77	down	0.00031
rc_AA232114_at	AA232114	463	epoxide hydrolase 2, cytoplasmic	24.34	down	0.00007
rc_AA233152_at	AA233152	467	EST	12.95	down	0
rc_AA233347_at	AA233347	470	zinc finger protein 216	5.9	down	0.0041
rc_AA233369_at	AA233369	471	histidine ammonia-lyase	9.06	down	0.0008
rc_AA233763_at	AA233763	472	EST	4.61	down	0.00004
rc_AA233837_at	AA233837	474	EST	4.79	down	0.0034
rc_AA234095_at	AA234095	478	EST	8.08	down	0.00394
rc_AA234527_s_at	AA234527	483	nuclear receptor subfamily 3, group C, member 1	6.19	down	0.00864
rc_AA234561_at	AA234561	485	EST	3.88	down	0.02058
rc_AA234634_f_at	AA234634	486	CCAAT/enhancer binding protein (C/EBP), delta	7.48	down	0.03318
rc_AA234817_at	AA234817	490	EST	6.22	down	0.00099
rc_AA234831_at	AA234831	491	EST	3.42	down	0.00206

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA234916_at	AA234916	492	EST	3.2	down	0.00799
rc_AA235233_at	AA235233	493	EST	6.59	down	0.00755
rc_AA235288_at	AA235288	494	PTPL1-associated RhogAP 1	3.7	down	0.00643
rc_AA235310_at	AA235310	496	EST	37.86	down	0.00091
rc_AA235507_at	AA235507	498	golgi autoantigen, golgin subfamily a, 5	3.28	down	0.00249
rc_AA235618_f_at	AA235618	499	EST	3.43	down	0.02127
rc_AA235765_s_at	AA235765	501	KIAA0214 gene product	3.59	down	0.01148
rc_AA235811_at	AA235811	502	EST	3.64	down	0.01272
rc_AA235873_s_at	AA235873	505	H factor (complement)-like 1,H factor 1	9.98	down	0.01667
rc_AA236230_at	AA236230	508	EST	5.28	down	0.01517
rc_AA236365_s_at	AA236365	509	3-phosphoglycerate dehydrogenase	10.23	down	0.00562
rc_AA236401_at	AA236401	510	EST	16.71	down	0.00088
rc_AA236455_f_at	AA236455	512	EST	15.71	down	0.00286
rc_AA236455_s_at	AA236455	512	EST	11.35	down	0.02859
rc_AA236796_s_at	AA236796	517	folistatin	8.74	down	0.00862
rc_AA236942_at	AA236942	519	EST	3.18	down	0.00862
rc_AA236982_at	AA236982	520	sterol carrier protein 2	5.56	down	0.01542
rc_AA242766_at	AA242766	523	EST	3.58	down	0.0151
rc_AA243495_at	AA243495	528	lectin, mannose-binding, 1	4.23	down	0.000179
rc_AA243582_at	AA243582	529	hemoglobin, gamma A	7.15	down	0.0021
rc_AA243595_s_at	AA243595	530	EST	3.11	down	0.008
rc_AA247453_at	AA247453	533	EST	3.09	down	0.0015
rc_AA250744_at	AA250744	536	EST	3.39	down	0.01137
rc_AA250775_at	AA250775	537	EST	4.52	down	0.01752
rc_AA251114_at	AA251114	539	prostate cancer overexpressed gene 1	6.6	down	0.00039
rc_AA251837_at	AA251837	547	EST	3.87	down	0.00782
rc_AA252289_at	AA252289	552	quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))	5.66	down	0.01389
rc_AA252365_at	AA252365	554	EST	3.9	down	0.01796
rc_AA253043_at	AA253043	559	DKFZP586I1419 protein	3.89	down	0.00145
rc_AA253129_at	AA253129	560	F-box protein FBL11	6.47	down	0.00001

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA253216_at	AA253216	EST	28.18	down	0.00141
rc_AA253369_s_at	AA253369	EST	15.59	down	0.00091
rc_AA253455_s_at	AA253455	EST	3.05	down	0.00533
rc_AA253459_at	AA253459	EST	4.51	down	0.00419
rc_AA255546_at	AA255546	EST	4	down	0.00301
rc_AA255624_at	AA255624	EST	4.06	down	0.00069
rc_AA255878_at	AA255878	KIAA0767 protein	3.96	down	0.00592
rc_AA255903_at	AA255903	CD39-like 4	5.67	down	0.01687
rc_AA256171_at	AA256171	EST	7.34	down	0.04562
rc_AA256341_at	AA256341	EST	7.37	down	0.00091
rc_AA256367_s_at	AA256367	paraoxonase 3	70.33	down	0.00192
rc_AA256666_at	AA256666	EST	4.63	down	0.0018
rc_AA257057_s_at	AA257057	EST	8.11	down	0.00379
rc_AA258308_at	AA258308	EST	5.4	down	0.00023
rc_AA258323_at	AA258323	EST	4.31	down	0.00046
rc_AA258350_at	AA258350	EST	5.08	down	0.00035
rc_AA258353_at	AA258353	EST	5.28	down	0.00193
rc_AA258567_at	AA258567	EST	6.92	down	0.00096
rc_AA258613_at	AA258613	EST	4.31	down	0.0344
rc_AA258813_at	AA258813	EST	4.63	down	0.02395
rc_AA259064_at	AA259064	EST	13.15	down	0.00001
rc_AA261954_at	AA261954	EST	7.69	down	0.00334
rc_AA262033_s_at	AA262033	EST	4.41	down	0.00054
rc_AA262349_at	AA262349	EST	3.78	down	0.00043
rc_AA262766_at	AA262766	EST	5.66	down	0.03832
rc_AA279112_at	AA279112	EST	3.42	down	0.01444
rc_AA279533_at	AA279533	EST	5.01	down	0.04448
rc_AA279550_at	AA279550	Kruppel-like factor	4.06	down	0.00957
rc_AA279676_s_at	AA279676	deoxyribonuclease I-like 3	23.35	down	0.00001
rc_AA279802_at	AA279802	EST	3.65	down	0.03366
rc_AA279937_at	AA279937	EST	3.38	down	0.02719

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
				4.12	down	0.00114
rc_AA280130_at	AA280130	636	EST spleen focus forming virus (SFFV) proviral	4.46	down	0.02062
rc_AA280413_s_at	AA280413	638	Integration oncogene spi1	3.11	down	0.03339
rc_AA280791_at	AA280791	640	eukaryotic translation initiation factor 5	6.43	down	0.01246
rc_AA281440_at	AA281440	644	EST	3.64	down	0.00002
rc_AA281545_at	AA281545	645	EST	3.23	down	0.00895
rc_AA281591_at	AA281591	646	DKFZP564M2423 protein	3.95	down	0.03606
AA281677_at	AA281677	648	seven in absentia (<i>Drosophila</i>) homolog 1	3.96	down	0.00094
rc_AA281770_at	AA281770	649	mannose-P-dolichol utilization defect 1	3.3	down	0.04108
rc_AA281796_at	AA281796	650	core-binding factor, runt domain, alpha subunit 2; translocated to, 3 KIAA0962 protein	3.27	down	0.02329
rc_AA281930_at	AA281930	651	KIAA0962 protein	8.95	down	0.01033
rc_AA282061_at	AA282061	652	EST	4.93	down	0.00108
rc_AA282089_at	AA282089	653	EST	3.09	down	0.01693
rc_AA282179_at	AA282179	655	EST	3.47	down	0.00677
rc_AA282238_at	AA282238	656	EST	7.67	down	0.00008
rc_AA282516_at	AA282516	660	7-dehydrocholesterol reductase	3.57	down	0.00049
rc_AA282886_at	AA282886	663	EST	4.37	down	0.03822
rc_AA282971_at	AA282971	665	EST	3.67	down	0.04293
rc_AA283758_at	AA283758	670	EST	3.09	down	0.00027
AA284558_at	AA284558	674	Nck, Ash and phospholipase C binding protein	3.34	down	0.03296
rc_aa284721_s_at	AA284721	677	EST	10.03	down	0.00019
rc_AA284785_at	AA284795	678	phosphatidylethanolamine N-methyltransferase	6.95	down	0.00125
rc_AA285053_at	AA285053	681	EST	3.66	down	0.00161
rc_AA287122_at	AA287122	686	DKFZP434C171 protein	3.53	down	0.00217
rc_AA287550_f_at	AA287550	689	KIAA0187 gene product	9.07	down	0.00013
rc_AA287566_at	AA287566	690	BCL2-interacting killer (apoptosis-inducing)	9.15	down	0.00514
rc_AA291323_at	AA291323	699	estrogen receptor 1	4.78	down	0.00059
rc_AA291749_s_at	AA291749	703	EST	5	down	0.00161
rc_aa292086_s_at	AA292086	705	EST	21.79	down	0.00031
AA292158_s_at	AA292158	706				

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA292328_at	AA292328	707	activating transcription factor 5	17.51	down	0.00689
rc_AA292711_at	AA292711	711	EST	3	down	0.01053
rc_AA292773_s_at	AA292773	713	collagen, type XVIII, alpha 1	7.44	down	0.00158
rc_AA293327_at	AA293327	716	isocitrate dehydrogenase 1 (NADP+), soluble	7.04	down	0.04377
rc_AA293485_at	AA293485	718	EST	3.36	down	0.02799
rc_AA298180_at	AA298180	726	EST	3.11	down	0.00747
rc_AA299632_at	AA299632	728	EST	4.23	down	0.00371
rc_AA312946_at	AA312946	731	EST	9.21	down	0.00106
AA314457_at	AA314457	733	synaptosomal complex protein 3	4.86	down	0.0013
rc_AA338512_at	AA338512	742	EST	3.05	down	0.03427
rc_AA342301_at	AA342301	746	EST	3.89	down	0.00038
rc_AA342337_at	AA342337	747	EST	3.87	down	0.0069
rc_AA342446_s_at	AA342446	748	insulin receptor	6.83	down	0.00412
rc_AA342771_at	AA342771	749	EST	5.33	down	0.00331
rc_AA343142_at	AA343142	751	EST	20.87	down	0.00003
rc_AA344866_s_at	AA344866	752	complement component 8, gamma polypeptide	7.28	down	0.00206
rc_AA347674_at	AA347674	753	EST	10.59	down	0.03716
rc_AA347717_at	AA347717	754	EST	5.25	down	0.00207
rc_AA348284_at	AA348284	755	EST	4.54	down	0.00759
rc_AA348466_s_at	AA348466	756	regulator of G-protein signalling 5	3.2	down	0.00571
rc_AA348485_at	AA348485	757	KIAA0438 gene product fatty-acid-Coenzyme A ligase, long-chain 1,fatty-	4.01	down	0.04563
rc_AA348922_s_at	AA348922	758	acid-Coenzyme A ligase, long-chain 2	64.27	down	0.00002
rc_AA349836_at	AA349836	760	EST	3.01	down	0.00911
rc_AA370359_s_at	AA370359	767	KIAA0382 protein; leukemia-associated rho guanine nucleotide exchange factor (GEF)	4.82	down	0.01077
rc_AA376875_at	AA376875	770	monoamine oxidase A	3.8	down	0.02746
rc_AA377087_at	AA377087	771	EST	16.75	down	0.00002
rc_AA381125_at	AA381125	772	EST	15.48	down	0
rc_AA382975_f_at	AA382975	773	EST	3.7	down	0.00131
rc_AA393825_at	AA393825	776	EST	3.62	down	0.0065

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
AA393961_at	AA3539861	EST	3.77	down	0.01029
AA397841_at	AA357841	EST	8.21	down	0
rc_AA397914_at	AA397914	EST	3.16	down	0.00336
rc_AA398102_at	AA388102	KIAA0429 gene product	6.22	down	0.00396
rc_AA398124_s_at	AA398124	growth factor receptor-bound protein 14	7.82	down	0.00009
rc_AA398221_at	AA398221	calcium/calmodulin-dependent protein kinase	3.78	down	0.00019
rc_AA398257_at	AA398257	7-dehydrocholesterol reductase	4.43	down	0.04169
rc_AA398280_at	AA398280	EST	12.43	down	0.00134
rc_AA398386_at	AA398386	EST	5.71	down	0.00007
rc_AA398422_at	AA398422	EST	3.94	down	0.00388
rc_AA398423_at	AA398423	EST	8.26	down	0.00063
rc_AA398445_at	AA398445	EST	4.28	down	0.01764
rc_AA398892_at	AA398892	similar to yeast BET3 (S. cerevisiae)	7.43	down	0.00038
rc_AA400030_at	AA400030	EST	3.98	down	0.00088
rc_AA400246_at	AA400246	mitogen-activated protein kinase-activated	3.09	down	0.00476
rc_AA400251_at	AA400251	EST	4.07	down	0.00032
rc_AA400258_at	AA400258	EST	11.89	down	0.00478
rc_AA400259_at	AA400259	EST	3.65	down	0.00476
rc_AA400471_at	AA400471	EST	5.45	down	0.0056
rc_AA400780_at	AA400780	EST	3.5	down	0.00107
rc_AA400831_at	AA400831	EST	3.49	down	0.00105
rc_AA400834_f_at	AA400834	EST	4.73	down	0.01523
rc_AA400864_at	AA400864	EST	7.51	down	0.02237
rc_AA400915_at	AA400915	EST	9.84	down	0.00351
rc_AA400934_at	AA400934	EST	4.98	down	0.02013
rc_AA400979_at	AA400979	calcitonin receptor-like receptor activity modifying	6.65	down	0.01051
rc_AA401151_at	AA401151	lyszyme (renal amyloidosis)	3.01	down	0.0051
rc_AA401343_at	AA401343	EST	3.11	down	0.01929
rc_AA401376_at	AA401376	EST	3.97	down	0.00797
rc_AA401562_s_at	AA401562	EST	50.45	down	0.00301
AA402006_at	AA402006	EST	4.19	down	0.00094

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
AA402095_s_at	AA402095	835 EST	3.12	down	0.01412
rc_AA402224_at	AA402224	836 growth arrest and DNA-damage-inducible,	14.41	down	0.00012
rc_AA402656_at	AA402656	841 EST	12.05	down	0.00001
rc_AA402799_at	AA402799	842 EST	11.81	down	0.00031
AA404252_at	AA404252	848 lectin, mannose-binding, 1	16.15	down	0.00001
rc_AA404352_at	AA404352	850 EST	7	down	0.00059
rc_AA404500_at	AA404500	852 EST	4.16	down	0.01375
rc_AA405819_at	AA405819	865 KIAA0668 protein	8.59	down	0.02034
rc_AA405832_at	AA405832	866 EST	12.24	down	0.00441
rc_AA405897_at	AA405907	867 EST	3.12	down	0
rc_aa406125_s_at	AA406125	868 EST	4.95	down	0.01027
rc_AA406126_at	AA406126	869 EST	8.43	down	0.00569
rc_AA406231_s_at	AA406231	873 KIAA0381 protein	4.46	down	0.04049
AA406435_at	AA406435	877 EST	3.24	down	0.00941
rc_AA410181_at	AA410181	881 EST	3	down	0.00268
rc_AA410255_at	AA410255	882 EST	7.56	down	0.00043
rc_AA410507_at	AA410507	884 EST	3.73	down	0.01703
rc_AA410523_at	AA410523	886 EST	6.37	down	0.03506
rc_AA411764_at	AA411764	891 similar to APOBEC1	4	down	0.01491
rc_AA412034_at	AA412034	894 EST	3.09	down	0.02309
rc_AA412063_at	AA412063	895 EST	8.26	down	0.00001
rc_AA412184_at	AA412184	898 EST	3.08	down	0.00012
rc_AA412481_s_at	AA412481	902 EST	8.07	down	0.00014
rc_AA416723_at	AA416723	906 EST	3.57	down	0.01042
rc_AA416740_at	AA416740	907 EST	3.08	down	0.01592
rc_AA416873_at	AA416873	908 EST	7.82	down	0.00005
rc_AA416880_s_at	AA416880	909 sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	6.6	down	0.00112
rc_AA416936_at	AA416936	910 5-methyltetrahydrofolate-homocysteine methyltransferase reductase	4.98	down	0.00632
rc_AA417046_at	AA417046	915 fatty-acid-Coenzyme A ligase, very long-chain 1	44	down	0

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA417078_at	AA417078	916	EST	4.1	down	0.00414
rc_AA417373_at	AA417373	917	EST	4.8	down	0.01342
rc_AA417375_at	AA417375	918	EST	4.21	down	0.00231
AA418098_at	AA418098	920	cAMP responsive element binding protein-like 2 cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1	3.18	down	0.03824
rc_AA418907_s_at	AA418907	922		4.05	down	0.04276
AA419507_at	AA419507	924	EST	5.58	down	0.00578
rc_AA419608_at	AA419608	925	EST	9.19	down	0.00005
rc_AA419622_at	AA419622	926	EST	4.62	down	0.00386
rc_AA421049_at	AA421049	927	activating transcription factor 5	44.41	down	0.00179
rc_AA421052_at	AA421052	929	branched chain alpha-ketoacid dehydrogenase	3.52	down	0.00869
rc_AA421244_s_at	AA421244	932	SH3-domain binding protein 5 (BTK-associated)	4.32	down	0.007
rc_AA421561_at	AA421561	933	insulin-like growth factor 2 (somatomedin A)	9.98	down	0.00007
AA424307_at	AA424307	944	EST	5.73	down	0.0074
rc_AA424672_s_at	AA424672	946	dermatopontin	4.69	down	0.00843
rc_AA424798_at	AA424798	947	EST	17.45	down	0.00352
rc_AA424813_at	AA424813	948	EST	5.77	down	0.00503
rc_AA425294_at	AA425294	952	EST	10.61	down	0.00083
rc_AA425309_at	AA425309	953	nuclear factor I/B	4.9	down	0.00466
rc_AA425782_at	AA425782	956	KIA0874 protein	5.52	down	0.03433
rc_AA425836_at	AA425836	957	EST	4.55	down	0.00035
AA426156_at	AA426156	959	EST	3.67	down	0.00153
AA426168_at	AA426168	960	KIA0805 protein	3.73	down	0.01477
AA426304_s_at	AA426304	962	EST	6.61	down	0.01092
rc_AA426330_at	AA426330	963	N-acylsphingosine amidohydrolase (acid	4.24	down	0.00668
rc_AA426468_at	AA426468	966	EST	3.38	down	0.0099
rc_AA426609_at	AA426609	968	EST	6.28	down	0.01233
rc_AA427778_at	AA427778	978	EST	3.57	down	0.00368
AA427783_at	AA427783	979	EST	4.37	down	0.0004
rc_AA427819_at	AA427819	980	midline 2	3.44	down	0.00063
AA428006_at	AA428006	984	DKFZP564B167 protein	3.71	down	0.02325

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA428150_at	AA428150	EST	5.24	down	0.00167
rc_AA428325_at	AA428325	EST	8.36	down	0.00002
rc_AA428567_at	AA428567	EST	3.99	down	0.00788
rc_AA428607_at	AA428607	ribosomal protein S5 pseudogene 1	4.21	down	0.04305
rc_AA428863_at	AA428863	EST	3.5	down	0.01726
rc_AA428900_at	AA428900	EST	7.01	down	0.00037
rc_AA429038_at	AA429038	EST	3.29	down	0.00927
rc_AA429478_at	AA429478	EST	3.41	down	0.02599
rc_AA429904_at	AA429904	EST	7.26	down	0.00524
AA430011_at	AA430011	EST	8.35	down	0.00729
rc_AA430026_at	AA430026	EST	3.31	down	0.00786
rc_AA430028_at	AA430028	EST	9.14	down	0.00246
rc_AA430044_at	AA430044	EST	7.78	down	0.00124
rc_AA430047_at	AA430047	EST	3.44	down	0.0016
rc_AA430108_at	AA430108	EST	3.8	down	0.04484
rc_AA430666_at	AA430666	EST	5.12	down	0.00377
rc_AA431337_at	AA431337	EST	6.26	down	0.00053
rc_AA431462_at	AA431462	EST	4.45	down	0.00956
rc_AA431480_s_at	AA431480	EST	4.3	down	0.00876
rc_AA431773_at	AA431773	EST	7.61	down	0.00063
rc_AA432168_at	AA432168	S-adenosylhomocysteine hydrolase-like 1	4.71	down	0.01377
rc_AA433946_at	AA433946	EST	43.74	down	0.00005
rc_AA435591_at	AA435591	kinesin family member 3B	3.5	down	0.0001
rc_AA435753_at	AA435753	EST	4.71	down	0.00078
rc_AA435777_f_at	AA435777	solute carrier family 25 (mitochondrial carrier), member 1	7.48	down	0.00613
rc_AA435824_at	AA435824	EST	3.93	down	0.02764
rc_AA435985_at	AA435985	EST	17.7	down	0
rc_AA436489_at	AA436489	EST	7.34	down	0.001
rc_AA436560_at	AA436560	claudin 1	11.41	down	0.00756
rc_AA436690_at	AA436690	EST	4.58	down	0.00948

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA436880_at	AA436880	1058	EST	3.22	down	0.00699
AA436926_at	AA436926	1059	EST	5.5	down	0.00984
rc_AA437235_s_at	AA437235	1060	EST	7.15	down	0.01455
rc_AA437265_s_at	AA437265	1061	EST	4.39	down	0.00826
rc_AA437295_at	AA437295	1062	ribosomal protein L7a	4.35	down	0.00347
rc_AA441791_at	AA441791	1065	EST	3.58	down	0.00357
AA442334_at	AA442334	1069	EST	7.15	down	0.00018
AA442342_at	AA442342	1070	EST	5.62	down	0.00052
AA443272_at	AA443272	1074	EST	7.68	down	0.00869
AA443658_at	AA443658	1079	transmembrane 7 superfamily member 2	9.06	down	0.00048
AA443756_at	AA443756	1080	EST	5.05	down	0.00341
rc_AA443822_at	AA443822	1082	EST	5.46	down	0.02538
rc_AA443934_at	AA443934	1083	GTP-binding protein Rho7	3.09	down	0.00214
AA443936	AA443936	1084	EST	22.96	down	0.00627
AA443993	AA443993	1086	EST	3.21	down	0.02948
AA446342_at	AA446342	1088	seven in absentia (<i>Drosophila</i>) homolog 1	4.84	down	0.00015
AA446587	AA446587	1091	EST	5.8	down	0.00012
AA446651	AA446651	1093	EST	3.14	down	0.01902
AA446666	AA446666	1094	EST	4.03	down	0.02369
rc_AA443936_s_at	AA443936	1095	UDP-N-acetylglucosamine pyrophosphorylase 1;			
rc_AA443993_at	AA443993	1096	Sperm associated antigen 2	6.37	down	0.02815
rc_AA446342_at	AA446342	1097	EST	3.26	down	0.04687
rc_AA446587_at	AA446587	1098	EST	3.22	down	0.02518
rc_AA446651_at	AA446651	1099	EST	8.08	down	0.00035
rc_AA446666_at	AA446666	1100	putative type II membrane protein	3.84	down	0.00045
rc_AA447549_at	AA447549	1101	FXYD domain-containing ion transport regulator 1	10.05	down	0
rc_AA447617_at	AA447617	1103	EST	3.87	down	0.00217
rc_AA447740_at	AA447740	1106	EST			
rc_AA447971_at	AA447971	1110	EST			
rc_AA447977_s_at	AA447977	1111	EST			
rc_AA448002_at	AA448002	1113	EST			
rc_AA448282_at	AA448282	1115	EST			
rc_AA448300_at	AA448300	1116	(phospholemm)	24.97	down	0.00001
rc_AA449267_at	AA449267	1120	EST	16.44	down	0.00926
rc_AA449297_at	AA449297	1121	EST	3.78	down	0.000039

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA449306_at	AA449306	1122	EST	5.01	down	0.0006
rc_AA449327_at	AA449327	1123	EST	4.77	down	0.01248
rc_AA449448_at	AA449448	1125	EST	3.97	down	0.00103
rc_AA450114_at	AA450114	1131	EST	4.96	down	0.01238
rc_AA450127_at	AA450127	1132	growth arrest and DNA-damage-inducible, beta	7.98	down	0.00078
rc_AA450281_at	AA450281	1134	EST	5.55	down	0.00004
rc_AA451836_at	AA451836	1137	EST	4.9	down	0.01412
rc_AA451911_at	AA451911	1139	EST	3.44	down	0.00221
rc_AA452158_at	AA452158	1141	ras homolog gene family, member B	28.96	down	0.00064
AA452454_at	AA452454	1144	EST	4.45	down	0.00179
rc_AA452549_at	AA452549	1146	platelet-derived growth factor receptor, alpha	3.3	down	0.04155
rc_AA452559_s_at	AA452559	1147	EST	4.35	down	0.00804
rc_aa452598_s_at	AA452598	1148	genethonin 1	5.49	down	0.00163
rc_AA452855_at	AA452855	1150	lectin, mannose-binding, 1	9.88	down	0.00428
rc_AA452860_at	AA452860	1151	EST	3.99	down	0.00831
rc_AA452915_at	AA452915	1152	EST	3.13	down	0.00561
rc_AA453770_s_at	AA453770	1157	EST	6.04	down	0.00524
AA453917_at	AA453917	1159	EST	3.3	down	0.01896
rc_AA453988_at	AA453988	1160	methionine adenosyltransferase I, alpha	54.29	down	0.00381
rc_AA454086_f_at	AA454086	1161	UDP-glucose dehydrogenase	4.29	down	0.00981
rc_AA454159_at	AA454159	1162	EST	10.81	down	0.00132
rc_AA454170_at	AA454170	1163	EST	3.11	down	0.03
rc_AA454177_i_at	AA454177	1164	EST	10.3	down	0.0008
rc_AA454184_at	AA454184	1165	EST	3.96	down	0.04605
rc_AA454733_s_at	AA454733	1169	EST	5.61	down	0.01182
rc_AA455097_i_at	AA455097	1172	EST	6.03	down	0.00419
rc_AA455367_at	AA455367	1176	DKFZP586F1018 protein	3.73	down	0.00202
AA455403_at	AA455403	1177	EST	15.46	down	0.01547
rc_AA455865_at	AA455865	1180	phosphatidylinositol glycan, class B	5.41	down	0.00004
rc_AA455896_s_at	AA455896	1181	glypican 1	3.46	down	0.00887
rc_AA455962_at	AA455962	1182	EST	3.1	down	0.03905

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
	AA455987	1183 EST	5.36	down	0.00029
rc_AA455988_at	AA455988	1184 butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase)	15.54	down	0.00001
rc_AA456055_at	AA456055	1185 EST	5.16	down	0.00158
rc_AA456147_at	AA456147	1188 general transcription factor IIIA	4.23	down	0.00088
rc_AA456289_at	AA456289	1189 EST	15.31	down	0.00004
rc_AA456311_s_at	AA456311	1190 EST	46.81	down	0.001
rc_AA456326_at	AA456326	1191 EST	3.35	down	0.00489
rc_AA456589_at	AA456589	1194 EST	4.23	down	0.00102
rc_AA456687_at	AA456687	1197 EST	3.08	down	0.01189
rc_AA457377_at	AA457377	1201 EST	3.1	down	0.00549
rc_AA458652_at	AA458652	1202 EST	8.26	down	0.00001
rc_AA458923_at	AA458923	1207 EST	3.36	down	0.00421
rc_AA458946_at	AA458946	1209 EST	15.88	down	0.00004
rc_AA459256_at	AA459256	1212 lectin, mannose-binding, 1	3.01	down	0.00094
rc_AA459293_at	AA459293	1213 EST	3.2	down	0.0001
rc_AA459389_at	AA459389	1216 tyrosylprotein sulfotransferase 2	3.72	down	0.02252
rc_AA459420_at	AA459420	1217 EST	7.25	down	0.0214
rc_AA459668_at	AA459668	1219 3-hydroxyisobutyryl-Coenzyme A hydrolase	7.62	down	0.00225
rc_aa459690_s_at	AA459690	1221 EST	9.18	down	0.00732
solute carrier family 22 (extraneuronal monoamine transporter), member 3					
rc_AA460012_at	AA460012	1224	4.27	down	0.04975
AA460047_at	AA460047	1226 EST	3.33	down	0.04011
AA460128_at	AA460128	1227 similar to S. pombe dim 1+	3.28	down	0.01299
rc_AA460449_at	AA460449	1228 EST	7.77	down	0.00011
rc_AA460661_at	AA460661	1229 EST	7.02	down	0.00053
rc_AA460916_at	AA460916	1233 EST	3.69	down	0.04841
rc_AA461057_at	AA461057	1234 nuclear localization signal deleted in	5.22	down	0.00051
rc_AA461303_at	AA461303	1238 DKFZP586D1519 protein	4.77	down	0.0438
rc_AA461444_at	AA461444	1239 EST	11.56	down	0.00167
rc_AA461458_at	AA461458	1241 EST	3.37	down	0.02427

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA463184_s_at	AA463194	1244	KIAA1037 protein	4.92	down	0.01866
rc_AA463195_at	AA463195	1245	EST	3.41	down	0.00413
AA463311_at	AA463311	1248	EST	3.71	down	0.04902
rc_AA463729_at	AA463729	1250	EST	4.07	down	0.00676
rc_AA463876_at	AA463876	1252	EST	0.00109	down	
rc_AA463946_at	AA463946	1254	pigment epithelium-derived factor	3.31	down	
rc_AA464188_s_at	AA464188	1256	EST	3.38	down	0.0018
rc_AA464603_at	AA464603	1260	EST	4.82	down	0.03208
rc_AA465240_at	AA465240	1270	EST	3.26	down	0.0007
rc_AA470153_at	AA470153	1275	solute carrier family 21 (organic anion	4.03	down	0.0046
rc_AA476324_s_at	AA476324	1281	EST	13.26	down	0.00315
rc_AA476346_at	AA476346	1283	EST	55.22	down	0.00132
rc_AA476352_at	AA476352	1284	EST	3.12	down	0.01067
rc_AA477119_at	AA477119	1289	EST	3.41	down	0.02233
AA477919_at	AA477919	1293	EST	3.13	down	0.0338
AA477978_s_at	AA477978	1294	short-chain dehydrogenase/reductase 1	4.69	down	0.00141
rc_AA478416_at	AA478416	1300	EST	8.53	down	0.01651
rc_AA478441_at	AA478441	1302	cathepsin F	4.04	down	0.00078
AA479132_at	AA479132	1309	EST	5.07	down	0.00752
rc_AA479148_at	AA479148	1311	EST	3.12	down	0.00876
rc_AA479488_at	AA479488	1313	S-adenosylhomocysteine hydrolase-like 1	38.05	down	0
rc_AA479498_at	AA479498	1314	EST	4	down	0.0269
rc_AA479885_at	AA479885	1318	KIAA0843 protein	5.78	down	0.01489
rc_AA479968_s_at	AA479968	1321	arylsulfatase A	15.57	down	0.00024
rc_AA480975_at	AA480975	1322	EST	9.01	down	0.00224
rc_AA480991_s_at	AA480991	1323	EST	8.95	down	0.00259
rc_AA481432_s_at	AA481432	1328	fibronectin 1	8.59	down	0.00156
rc_AA481526_at	AA481526	1329	EST	7.76	down	0.0061
AA481670_at	AA481670	1330	retinal short-chain dehydrogenase/reductase	3.73	down	0.00002
rc_AA482594_at	AA482594	1337	EST	6.2	down	0.0078
rc_AA485089_at	AA485089	1341	EST	5.42	down	0.00387
				5.46	down	0.00044

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA485326_at	AA485326	1342	ATP-binding cassette, sub-family D (ALD),	3.08	down	0.00415
rc_AA485413_at	AA485413	1344	EST	4.54	down	0.00137
rc_AA486410_at	AA486410	1348	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	8.08	down	0.00485
rc_AA486511_at	AA486511	1349	EST	22.21	down	0.00113
rc_AA486567_at	AA486567	1350	EST	5	down	0.00002
rc_AA487161_at	AA487161	1353	ubiquilin 2	3.13	down	0.00023
rc_AA487503_at	AA487503	1356	EST	8.85	down	0.00012
rc_AA487606_at	AA487606	1358	EST	3.05	down	0.00291
rc_AA488843_at	AA488843	1362	cornichon-like	8.58	down	0.02131
rc_AA489061_at	AA489061	1367	EST	3.49	down	0.00223
rc_AA489629_at	AA489629	1369	EST	8.08	down	0.00109
rc_AA489636_at	AA489636	1370	EST	10.7	down	0
rc_AA489798_at	AA489798	1373	hypothetical protein, estradiol-induced	8.75	down	0.00544
rc_AA490159_at	AA490159	1374	glucose-6-phosphatase, transport (glucose-6-	5.44	down	0
rc_AA49214_at	AA49214	1376	EST	3.12	down	0.02382
rc_AA490620_at	AA490620	1378	EST	4.77	down	0.00201
rc_AA490670_at	AA490670	1379	EST	9.96	down	0.00454
AA490775_at	AA490775	1380	UDP-N-acetylglucosamine-2-epimerase/N-	5.34	down	0.00118
rc_AA490882_s_at	AA490882	1381	acetylmannosamine kinase	3.29	down	0.00319
rc_AA490890_at	AA490890	1382	EST	3.02	down	0.00007
rc_AA491000_at	AA491000	1385	EST	4.23	down	0.02305
rc_AA491001_f_at	AA491001	1386	EST	8.52	down	0.01118
rc_AA491001_f_at	AA491001	1386	EST	3.73	down	0.01957
rc_AA495758_s_at	AA495758	1391	EST	3.94	down	0.00772
rc_AA495820_at	AA495820	1393	EST	3.98	down	0.00218
rc_AA496053_at	AA496053	1396	EST	3.28	down	0.00095
rc_AA496423_at	AA496423	1399	WW domain binding protein 2	3.52	down	0.01314
rc_AA496914_at	AA496914	1401	v-maf musculoaponeurotic fibrosarcoma (avian)	3.48	down	0.00361
rc_AA497052_at	AA497052	1408	DKFZP727G051 protein	7.28	down	0.01745

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA504492_at	AA504492	1414	tubulin, alpha, ubiquitous	4.21	down	0.00752
AA505198_at	AA505198	1419	EST	3.41	down	0.0343
rc_AA521290_at	AA521290	1421	EST	4.53	down	0.0148
rc_AA521292_at	AA521292	1422	EST	8.58	down	0.00064
rc_AA521306_at	AA521306	1423	EST	4.27	down	0.00567
rc_AA598417_at	AA598417	1426	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	8.56	down	0.01638
rc_AA598419_s_at	AA598419	1427	translational inhibitor protein p14.5	23.6	down	0.00036
rc_AA598675_at	AA598675	1433	EST	3.25	down	0.03934
rc_AA598679_at	AA598679	1434	EST	5.37	down	0.00467
rc_AA598746_at	AA598746	1437	EST	3.8	down	0.02667
rc_AA598926_at	AA598926	1441	EST	3.7	down	0.00432
rc_AA599211_at	AA599211	1445	short-chain dehydrogenase/reductase 1	7.85	down	0.00911
rc_AA599234_s_at	AA599234	1447	murine leukemia viral (bml-1) oncogene homolog	3.9	down	0.0068
rc_AA599472_at	AA599472	1451	succinate-CoA ligase, GDP-forming, beta subunit	5.07	down	0.00447
rc_AA599526_at	AA599526	1453	cartilage associated protein	3.02	down	0.00043
rc_AA599814_at	AA599814	1456	EST	12.37	down	0.00002
rc_AA599937_s_at	AA599937	1458	insulin-like growth factor-binding protein 4	26.92	down	0.00094
rc_AA599954_at	AA599954	1459	cell cycle progression 8 protein	3.15	down	0.00021
rc_AA608546_at	AA608546	1463	EST	12.52	down	0.00003
rc_AA608671_at	AA608671	1466	EST	3.14	down	0.04543
rc_AA608729_at	AA608729	1468	EST	3.89	down	0.01757
rc_AA608751_1_at	AA608751	1469	EST	5.76	down	0.01404
rc_AA608802_at	AA608802	1470	EST	6.95	down	0.00263
rc_AA608807_s_at	AA608807	1471	Inhibin, beta B (activin AB beta polypeptide)	4.05	down	0.00568
rc_AA608837_at	AA608837	1472	EST	6.2	down	0.00006
rc_AA609011_at	AA609011	1476	EST	3.94	down	0.0313
rc_AA609164_at	AA609164	1480	cytochrome b-561	6.8	down	0.02298
rc_AA609316_at	AA609316	1481	EGF-like-domain, multiple 5	7.97	down	0.00011
rc_AA609519_at	AA609519	1482	EST	8.13	down	0.00009
rc_AA609537_s_at	AA609537	1483	hepatic leukemia factor	8.76	down	0.00018

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
rc_AA609572_at	AA609572	1484	EST	3.02	down	0.01534
rc_AA609574_at	AA609574	1485	EST	5.03	down	0
rc_AA609576_at	AA609576	1486	EST	3.1	down	0.00266
rc_AA609773_at	AA609773	1489	EST	6.09	down	0.01103
rc_AA609774_at	AA609774	1490	EST	4.02	down	0.00424
rc_AA609934_at	AA609934	1493	EST	6.84	down	0.00048
rc_AA609996_at	AA609996	1495	EST	3.93	down	0.00988
rc_AA620343_at	AA620343	1500	EST	5.04	down	0.00407
rc_AA620556_at	AA620556	1505	EST	32.4	down	0.00353
rc_AA620667_s_at	AA620667	1506	protein tyrosine phosphatase type IVA, member 1	5.92	down	0.00206
rc_AA620830_at	AA620830	1509	DKFZP564I122 protein	3.42	down	0.02421
rc_AA621131_at	AA621131	1513	EST	35.37	down	0
rc_AA621192_at	AA621192	1515	EST	5.39	down	0.0016
rc_AA621209_at	AA621209	1516	similar to <i>Caenorhabditis elegans</i> protein	6.34	down	0.00144
rc_AA621235_at	AA621235	1517	EST	3.44	down	0.0021
rc_AA621274_1_at	AA621274	1519	EST	7.43	down	0.00065
rc_AA621430_at	AA621430	1525	doublecortex; lissencephaly, X-linked	3.09	down	0.00024
rc_AA621796_at	AA621796	1531	kinesin family member 3B	4.44	down	0.00032
			PDZ domain containing guanine nucleotide exchange factor(GEF)1; RA(Ras/Rap1A-binding protein 1	4.21	down	0.00476
AB002311_at	AB002311	1535		5.55	down	0.00016
AB002328_at	AB002328	1536	calcineurin binding protein 1	13.76	down	0.00002
AF000573_rna1_at	AF000573	1543	homogenibate 1,2-dioxygenase (homogenibate secretory carrier membrane protein 3	3.42	down	0.04953
AF005039_at	AF005039	1548	solute carrier family 4, sodium bicarbonate cotransporter, member 4	5.79	down	0.00005
AF007216_at	AF007216	1550		5.35	down	0.00608
C01257_at	C01257	1554	EST	4.11	down	0.00292
C01286_s_at	C01286	1555	integral membrane protein 2B	4.41	down	0.01725
C01409_s_at	C01409	1556	EST	3.01	down	0.00048
C01686_at	C01686	1557	EST	5.85	down	0.02377
C02099_s_at	C02099	1560	CG-131 protein	3.64	down	0.02705
C02460_at	C02460	1562	EST			

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_C14963_s_at	C14963	1572	nicotinamide nucleotide transhydrogenase	3.9	down	0.0044
C15871_at	C15871	1575	EST	3.26	down	0.00046
C16420_s_at	C16420	1576	EST	5.95	down	0.00119
rc_C20653_at	C20653	1578	EST	10.59	down	0.00001
rc_C20810_at	C20810	1579	EST	5.17	down	0.00614
rc_C20911_at	C20911	1580	antithrombin III	6.56	down	0.00175
rc_C20974_at	C20974	1581	Vavin 1	6.66	down	0.00272
rc_C21130_at	C21130	1583	EST	8.79	down	0.00008
rc_C21238_at	C21238	1584	EST	4.54	down	0.02074
D00003_s_at	D00003	1586	cytochrome P450, subfamily IIIA (nphedipine oxidase), polypeptide 3	22.05	down	0.000059
D00003_at	D00003	1586	cytochrome P450, subfamily IIIA (nphedipine oxidase), polypeptide 3	9.46	down	0.00001
D00097_s_at	D00097	1588	amyloid P component, serum	16.72	down	0.00098
D00408_s_at	D00408	1589	cytochrome P450, subfamily IIIA (nphedipine oxidase), polypeptide 5, cytochrome P450, subfamily IIIA (nphedipine oxidase)	11.1	down	0
D00632_at	D00632	1591	glutathione peroxidase 3 (plasma)	6.55	down	0.00121
D00723_at	D00723	1592	glycine cleavage system protein H (aminomethyltransferase)	4.18	down	0.00543
D10040_at	D10040	1593	fatty-acid-Coenzyme A ligase, long-chain 2	20.51	down	0
D10511_at	D10511	1594	acyetyl-Coenzyme A acetyltransferase 1 (acetooacetyl Coenzyme A thiolase)	10.68	down	0.0002
rc_D11756_f_at	D11756	1596	EST	5.49	down	0.01272
rc_D11802_at	D11802	1597	angiotensinogen	5.65	down	0.00009
rc_D11835_at	D11835	1598	low density lipoprotein receptor (familial)	21.76	down	0.00307
rc_D11881_at	D11881	1599	KIAA0962 protein	4.37	down	0.01627
D12485_at	D12485	1600	phosphodiesterase 1/nucleotide pyrophosphatase 1 (homologous to mouse Ly-41 antigen)	4.57	down	0.00008

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	P value
D12620_s_at	D12620	cytochrome P450, subfamily IVF, polypeptide 3 2, cytochrome P450, subfamily IVF, polypeptide 3	35.09	down	0.000015
D12620_s_at	1601	(leukotriene B4 omega hydroxylase)	0		
D13243_s_at	1601	cytochrome P450, subfamily IVF, polypeptide 3 2, cytochrome P450, subfamily IVF, polypeptide 3	13.45	down	0
D13643_at	1602	(leukotriene B4 omega hydroxylase)	20.22	down	0
D13705_s_at	1609	pyruvate kinase, liver and RBC	10.84	down	0.000058
D13814_s_at	1610	KIAA0018 gene product	3.7	down	0.000038
D14012_s_at	1611	cytochrome P450, subfamily IVA, polypeptide 11	3.12	down	0.00101
D14664_at	1612	angiotensin receptor 1, angiotensin receptor 1B	12.75	down	0.0035
D14695_at	1616	HGF activator	8.98	down	0.00011
D16294_at	1618	KIAA0022 gene product	6.48	down	0
D16350_at	1619	KIAA0025 gene product; MMS-inducible gene	4.81	down	0.03921
D16481_at	1620	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	3.83	down	0.00117
D16626_at	1621	SA (rat hypertension-associated) homolog	3.18	down	0.00695
D16626_at	1622	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	22.66	down	0
rc_D20350_at	1622	histidine ammonia-lyase	9.25	down	0.00025
D31117_at	1624	EST	13.97	down	0.00057
D31225_at	1640	ribosome binding protein 1 (dog 180kD homolog)	5.3	down	0.02749
D31289_at	1641	EST	3.17	down	0.01073
D31381_at	1642	EST	4.16	down	0.02166
D31628_s_at	1644	dynamin, axonemal, light polypeptide 4	4.97	down	0.01806
D31716_at	1646	4-hydroxyphenylpyruvate dioxygenase	50.48	down	0.00002
D31815_at	1647	basic transcription element binding protein 1	5.35	down	0.00086
D31887_at	1648	regucalcin (senescence marker protein-30)	10.55	down	0.00037
D37931_at	1649	KIAA0062 protein	4.26	down	0.00101
	1650	ribonuclease, RNase A family, 4	5.81	down	0.00836

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
D38535_at	D38535	1654	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)	13.2	down	0.01165
rc_D45529_at	D45529	1662	EST	3.82	down	0.00193
rc_D45556_at	D45556	1663	EST	4.83	down	0.01044
rc_D45714_at	D45714	1664	EST	5.64	down	0.00384
D49357_at	D49357	1665	methionine adenosyltransferase I, alpha	11.28	down	0.00331
D49387_at	D49387	1666	NADP dependent leukotriene b4 12-hydruronan-binding protein 2	8.17	down	0.00972
D49742_at	D49742	1668	hyaluronan-binding protein 2	18.13	down	0.00012
rc_D51199_at	D51199	1677	EST	5.05	down	0.00192
rc_D51279_s_at	D51279	1679	ovarian granulosa cell protein (13kD)	5.88	down	0.01271
rc_D52097_s_at	D52097	1682	prostatic binding protein	8.1	down	0.00141
D57823_at	D57823	1690	Sec23 (S. cerevisiae) homolog A	4.43	down	0
D58231_s_at	D58231	1692	ubiquitin-like 3	3.07	down	0.0002
rc_D59344_s_at	D59344	1695	EST	3.34	down	0.01337
rc_D59554_f_at	D59554	1698	EST	6.7	down	0
rc_D59714_s_at	D59714	1700	mitogen inducible 2	17.62	down	0.00014
rc_D60670_at	D60670	1702	EST	3.73	down	0.00382
rc_D60769_s_at	D60769	1703	KIAA0096 protein	4.31	down	0.00142
rc_D60856_f_at	D60856	1705	UDP-glucose dehydrogenase	6.45	down	0.01222
D61991_at	D61991	1706	EST	4.84	down	0.00005
D62103_s_at	D62103	1707	EST	4.11	down	0.0263
rc_D62518_at	D62518	1708	EST	17.49	down	0.00017
D63160_at	D63160	1709	ficolin (collagen/fibrinogen domain-containing dihydroprymidinase	4.01	down	0.00391
D78011_at	D78011	1717	succinate-CoA ligase, GDP-forming, beta subunit	21.37	down	0.00003
D79276_at	D79276	1722	KIAA1053 protein	6.8	down	0.00047
D79687_at	D79687	1723	dihydroprymidinase	5.06	down	0.00047
rc_D80050_at	D80050	1726	EST	4.64	down	0.01001
rc_D80217_f_at	D80217	1727	H91620p protein	3.61	down	0.01973
rc_D80218_f_at	D80218	1728	brain acid-soluble protein 1	3.83	down	0.0137
rc_D80312_f_at	D80312	1730	EST	3.74	down	0.01909
rc_D80408_at	D80408	1731	EST	3.36	down	0.00102

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_D80905_at	D80905	1735	EST	3.59	down	0.00007
D82061_at	D82061	1741	Kef6 gene, mouse, human homolog of ferroportin 1; iron regulated gene 1	6.1	down	0.00104
D82422_at	D82422	1745	sterol-C5-desaturase (fungal ERG3, delta-5-	6.01	down	0.02351
D85181_at	D85181	1750	ES1 (zebrafish) protein, human homolog of solute carrier family 23 (nucleobase transporters),	9.56	down	0.00005
D86062_s_at	D86062	1752	KIAA0249 gene product	3.63	down	0.0001
D87075_at	D87075	1760	KIAA0260 protein	4.15	down	0.000067
D87436_at	D87436	1761	KIAA0276 protein	5.49	down	0.000333
D87449_at	D87449	1762	N-acetyltransferase 2 (arylamine N-carbamoyl-phosphate synthetase 1, mitochondrial	4.58	down	0.000026
D87466_at	D87466	1763	EST	4.83	down	0.00007
D90042_at	D90042	1767	ectropic viral Integration site 5	7.06	down	0
D90282_at	D90282	1769	monoamine oxidase A	27.29	down	0.00002
F02028_at	F02028	1774	EST	23.48	down	0.00465
rc_F02094_at	F02094	1775	matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase)	3.41	down	0.00495
rc_F02245_at	F02245	1776	EST	3.9	down	0.02943
rc_F02345_at	F02345	1779	EST	3.9	down	0.0033
rc_F03200_at	F03200	1783	EST	3.75	down	0.01805
rc_F03969_at	F03969	1785	EST	7.87	down	0.00014
rc_F04335_at	F04335	1787	EST	3.16	down	0.00058
rc_F04611_at	F04611	1792	EST	23.96	down	0.00018
rc_F04944_s_at	F04944	1795	acyl-Coenzyme A oxidase	4.01	down	0.00242
rc_F08817_at	F08817	1796	EST	8.29	down	0.0077
rc_F08941_at	F08941	1798	EST	3.48	down	0.00428
rc_F09058_at	F09058	1799	EST	3.6	down	0.00595
rc_F09350_at	F09350	1801	EST	4.79	down	0.00088
rc_F09353_at	F09353	1802	solute carrier family 5 (inositol transporters), core-binding factor, runt domain, alpha subunit 2; translocated to, 3	3.3	down	0.02841
rc_F09578_at	F09578	1804	EST	4.66	down	0.04463
rc_F09979_at	F09979	1809	hepsin (transmembrane protease, serine 1)	4.36	down	0.02555
rc_F10182_s_at	F10182	1812	dual specificity phosphatase 6	58.92	down	0.00837
rc_F10276_s_at	F10276	1814	EST	8.13	down	0.00001

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_F10466_at	F10466	1820	EST	5.32	down	0.02494
rc_F10640_at	F10640	1821	EST	3.58	down	0.00152
rc_F10874_f_at	F10874	1823	EST	4.19	down	0.00025
rc_F10875_at	F10875	1824	EST	5.09	down	0.00004
rc_F13702_at	F13702	1826	EST	6.01	down	0.00064
rc_F13782_s_at	F13782	1827	LIM binding domain 2 TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	4.17	down	0.00109
rc_H02848_s_at	H02848	1831		3.47	down	0.0089
rc_H02855_at	H02855	1832	EST	5.96	down	0.00458
rc_H03348_at	H03348	1833	claudin 1	5.77	down	0.0001
rc_H03945_at	H03945	1835	EST	4.94	down	0.02603
rc_H04142_f_at	H04142	1836	EST	3.57	down	0.01906
rc_H04242_at	H04242	1837	RAB5B, member RAS oncogene family	3.27	down	0.04826
H04854_at	H04854	1842	interleukin 1 receptor accessory protein	6.58	down	0.00007
rc_H05072_at	H05072	1843	EST	3.12	down	0.01248
rc_H05974_s_at	H05974	1850	EST	6.28	down	0.00549
rc_H05985_at	H05985	1851	hypothetical protein	6.43	down	0.04887
rc_H06063_s_at	H06063	1852	chondroitin sulfate proteoglycan 3 (neurocan)	3.15	down	0.00589
rc_H06144_at	H06144	1853	EST	3.1	down	0.00745
rc_H06166_at	H06166	1854	EST	3.31	down	0.03778
rc_H06935_s_at	H06935	1855	electron-transferring-flavoprotein dehydrogenase	6.82	down	0.00105
rc_H08054_at	H08054	1857	EST	4.2	down	0.00009
rc_H08102_at	H08102	1858	breast cell glutaminase	27.77	down	0.00032
rc_H09167_at	H09167	1860	KIAA0195 gene product	3.31	down	0.00313
rc_H09353_at	H09353	1866	EST	23.06	down	0.00094
H09364_s_at	H09364	1867	succinate dehydrogenase complex, subunit A,	5.74	down	0.03125
rc_H09594_at	H09594	1868	EST	3.12	down	0.00231
rc_H09959_s_at	H09959	1869	choline kinase	3.25	down	0.00225
H10482_at	H10482	1870	EST	3.19	down	0.01611
rc_H10661_at	H10661	1871	EST	4.54	down	0.00276

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_H10779_s_at	H10779	1872	methyltetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	9.73	down	0.00035
rc_H11274_at	H11274	1874	EST	4.13	down	0.01478
rc_H11739_s_at	H11739	1876	glycine dehydrogenase (decarboxylating; glycine cleavage system protein	10.33	down	0.00023
rc_H11746_at	H11746	1877	EST	3.92	down	0.00012
rc_H12257_at	H12257	1879	EST	3.19	down	0.0069
rc_H12593_at	H12593	1880	zinc-finger protein 265	10.72	down	0.0056
rc_H13696_at	H13696	1882	EST	3.48	down	0.01796
rc_H14372_s_at	H14372	1883	ATP-binding cassette, sub-family A (ABC1),	5.16	down	0.00012
rc_H16768_at	H16768	1887	EST	3.72	down	0.00688
rc_H18950_at	H18950	1892	EST	3.85	down	0.00162
rc_H18997_at	H18997	1893	F-box protein 21	3.87	down	0.00611
rc_H19504_f_at	H19504	1895	EST	3.13	down	0.04948
rc_H20543_at	H20543	1897	DKFZP586B1621 protein	31.03	down	0.00074
rc_H25124_at	H25124	1903	EST	3.65	down	0.0004
rc_H25551_at	H25551	1904	EST	3.54	down	0.00366
rc_H25836_at	H25836	1905	tumor necrosis factor (ligand) superfamily,	3.3	down	0.03125
rc_H26417_at	H26417	1906	EST	3.22	down	0.03672
rc_H26763_at	H26763	1907	EST	3.39	down	0.04188
rc_H27330_at	H27330	1909	EST	3.2	down	0.00067
rc_H27442_s_at	H27442	1910	erythrocyte membrane protein band 7.2	6.81	down	0.00083
rc_H29568_at	H29568	1914	EST	11.45	down	0.00058
rc_H30270_at	H30270	1915	EST	17.09	down	0.00001
rc_H38246_s_at	H38246	1917	EST	9.25	down	0.00157
rc_H39119_at	H39119	1919	EST	3.06	down	0.03349
rc_H40149_at	H40149	1921	KIA0937 protein	4.59	down	0.00112
rc_H40424_s_at	H40424	1922	butyrate response factor 1 (EGF-response factor	3.56	down	0.04066
rc_H40534_at	H40534	1923	EST	3.18	down	0.01381
rc_H41084_at	H41084	1924	EST	6.31	down	0.0227

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_H41280_at	H41280	1925	EST	3.68	down	0.00455
rc_H42053_s_at	H42053	1927	EST	3.49	down	0.01057
rc_H46001_at	H46001	1931	EST	5.03	down	0.00563
rc_H46990_at	H46990	1933	cytochrome P450, subfamily IIE (ethanol-	3.2	down	0.00095
rc_H47391_at	H47391	1935	EST	3.1	down	0.03807
rc_H47838_at	H47838	1936	carboxypeptidase B2 (plasma)	16.74	down	0.00002
rc_H49415_at	H49415	1938	EST	3.72	down	0.0005
rc_H51340_at	H51340	1941	EST	3.73	down	0.02643
rc_H54285_s_at	H54285	1947	EST	5.14	down	0.00426
rc_H55759_at	H55759	1949	EST	11.52	down	0.00034
rc_H56584_at	H56584	1951	neuronal SNAP25-like 1	9.5	down	0
rc_H57060_s_at	H57060	1954	EST	30.98	down	0.01687
rc_H57166_at	H57166	1955	EST	60.76	down	0.00007
rc_H57816_at	H57816	1957	EST	4.41	down	0.00206
rc_H57850_at	H57850	1958	protein phosphatase 2 (formerly 2A), regulatory			
rc_H58673_at	H58673	1959	subunit A (PR 65), beta isoform	3.02	down	0.00123
rc_h58692_s_at	H58692	1960	formyltetrahydrofolate dehydrogenase	14.85	down	0.00005
rc_H59136_at	H59136	1962	EST	81.41	down	0
rc_H59141_at	H59141	1963	EST	8.64	down	0.00013
rc_H60595_s_at	H60595	1966	progesterone binding protein	3.12	down	0.00293
H61295_s_at	H61295	1968	CD4 antigen (p55)	15.8	down	0.01078
rc_H62838_at	H62838	1971	EST	10.71	down	0.00925
rc_H63251_at	H63251	1972	KIAA0606 protein; SCN Circadian Oscillatory	3.09	down	0.03201
rc_H65650_at	H65650	1976	EST	3.27	down	0.02455
H66367_at	H66367	1977	EST	3.88	down	0.00083
rc_H66840_at	H66840	1978	EST	6.68	down	0.0001
rc_H67094_at	H67094	1979	EST	3.67	down	0.0143
H67840_at	H67840	1980	EST	3.24	down	0.00075
rc_H68097_at	H68097	1982	EST	3.1	down	0.00528
				3.83	down	0.00797

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
H68953_at	H68953	1985	transferrin	6.4	down	0.00132
rc_H69138_at	H69138	1986	v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene	6.76	down	0.00142
rc_H69565_at	H69565	1987	EST	4.11	down	0.00002
rc_H70554_at	H70554	1989	EST	10.99	down	0
rc_H71169_at	H71169	1992	putative protein similar to nessy (Drosophila)	4	down	0.00709
rc_H71861_s_at	H71861	1993	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease,	5.97	down	0.00007
rc_H73535_s_at	H73535	1996	EST	6.89	down	0.00202
rc_H74317_s_at	H74317	1997	apolipoprotein A-II	45.09	down	0.01982
rc_H77597_f_at	H77597	2000	metallothionein 1H	16.03	down	0.00675
rc_H78628_at	H78628	2003	EST	4.98	down	0.00729
rc_H79820_at	H79820	2004	EST	3.25	down	0.01466
rc_H80901_s_at	H80901	2005	ficolin (collagen/fibrinogen domain-containing) 3	50.61	down	0.00262
rc_H81070_f_at	H81070	2006	RNA helicase-related protein	25.74	down	0.00126
rc_H82966_s_at	H82966	2011	apolipoprotein B (including Ag(x) antigen)	3.42	down	0.00769
rc_H83109_f_at	H83109	2012	EST	16.55	down	0.00001
rc_H83442_s_at	H83442	2013	catechol-O-methyltransferase	3.99	down	0.00594
rc_H83451_at	H83451	2014	EST	3.35	down	0.00498
rc_H87144_at	H87144	2016	EST	3.41	down	0.00387
rc_H87765_at	H87765	2017	KIAA0626 gene product	3.86	down	0.00131
rc_H88033_s_at	H88033	2019	KIAA0733 protein	4.42	down	0.02032
rc_H88359_s_at	H88359	2020	nuclear factor (erythroid-derived 2)-like 2	5.16	down	0.01253
rc_H88675_at	H88675	2022	EST	5.63	down	0.00554
rc_H89514_s_at	H89514	2023	protein kinase, cAMP-dependent, catalytic, alpha	3.44	down	0.00435
rc_H89893_at	H89893	2025	EST	3.17	down	0.00658
rc_H89980_at	H89980	2026	protein phosphatase 1, regulatory (inhibitor)	31.13	down	0.00006
rc_H90417_s_at	H90417	2028	EST	4.17	down	0.015
rc_H91325_s_at	H91325	2029	aldolase B, fructose-bisphosphate	45.85	down	0.00505
rc_H91456_s_at	H91456	2030	nuclear receptor subfamily 1, group H, member 4 phosphorylase, glycogen; liver (Hers disease,	4.9	down	0.00255
rc_H91680_s_at	H91680	2032	glycogen storage disease type VI)	4.15	down	0.00746

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_H93053_s_at	H93053	2034	glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD)	5.06	down	0.01029
H93246_s_at	H93246	2035	EST	15.3	down	0.00233
rc_H93381_at	H93381	2036	EST	24.23	down	0
rc_H93562_at	H93562	2038	proline synthetase co-transcribed (bacterial 3-hydroxy-3-methylglutaryl-Coenzyme A synthase	3.17	down	0.00113
rc_H94247_s_at	H94247	2041	2 (mitochondrial)	9.49	down	0.02373
rc_H94475_s_at	H94475	2043	alpha-2-plasmin inhibitor	40.92	down	0.00271
rc_H94648_at	H94648	2044	EST	4.77	down	0.00266
rc_H94666_at	H94666	2045	alpha-1-B glycoprotein	47.03	down	0.01158
rc_H95358_at	H95358	2049	EST	3.17	down	0.00182
rc_H95569_l_at	H95569	2051	DKFZP586A0522 protein	28.48	down	0.00139
rc_H95978_at	H95978	2052	EST	8.55	down	0.00046
rc_H96614_at	H96614	2054	EST	4.02	down	0.01565
rc_H97868_at	H97868	2064	EST	3.86	down	0.00362
rc_H97986_at	H97986	2065	EST	3.86	down	0.01534
rc_H98071_at	H98071	2066	EST	4.66	down	0.03722
rc_H98083_at	H98083	2067	EST	5.09	down	0.00025
rc_H98771_l_at	H98771	2069	BCL2/adenovirus E1B 19kD-interacting protein 3	8	down	0.00118
rc_H98822_at	H98822	2070	EST	3.31	down	0.00174
rc_H98910_s_at	H98910	2071	EST	4.38	down	0.00548
rc_H98977_at	H98977	2073	EST	3.57	down	0.00298
rc_H99393_s_at	H99393	2076	endothelin receptor type B	3.43	down	0.00093
rc_H99727_at	H99727	2080	adipose differentiation-related protein; adipophilin	5.83	down	0.04346
rc_H99935_s_at	H99935	2085	interleukin 6 signal transducer (gp130, oncostatin	3.59	down	0.00366

Table 6B. Down regulated *in metastatic cancers versus normal sample set 2.*

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
J02843_at	J02843	cytochrome P450, subfamily IIE (ethanol-NAD(P)H menadione oxidoreductase 2, dioxin-corticosteroid binding globulin)	22.58	down	0.00935
J02868_at	J02868	NAD(P)H menadione oxidoreductase 2, dioxin-Insulin-like growth factor 2 (somatomedin A)	3.15	down	0.02385
J02943_at	J02943	complement component 7	18.98	down	0.00087
J03242_s_at	J03242	complement component 7	4.01	down	0.00042
J03507_at	J03507	plasminogen activator inhibitor, type I	3.77	down	0.00184
J03764_at	J03764	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	5.6	down	0.02196
J03805_s_at	J03805	solute carrier family 2 (facilitated glucose	3.87	down	0.0116
J03810_at	J03810	EST	21.99	down	0.00004
J03910_ma1_at	J03910	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	12.42	down	0.01167
J04031_at	J04031	carboxyl reductase 1	3.4	down	0.00786
J04056_at	J04056	complement component 1, s subcomponent	5.19	down	0.00001
J04080_at	J04080	UDP glycosyltransferase 1	5.48	down	0.0239
J04093_s_at	J04093		18.92	down	0

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
J04093_s_at	J04093	2106 UDP glycosyltransferase 1 cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 3	18.92	down	0
J04449_at	J04449	2110 SNRPN upstream reading frame	5.25	down	0.01583
J04615_at	J04615	2112 syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)	3.14	down	0.02928
J04621_at	J04621	2113 cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 5	3.38	down	0.00275
J04813_s_at	J04813	2114 serine dehydratase	9.67	down	0.0107
J05037_at	J05037	2116 carboxypeptidase N, polypeptide 2, 83kD	16.24	down	0.00015
J05158_at	J05158	2117 UDP glycosyltransferase 2 family, polypeptide B7	8.52	down	0
J05428_at	J05428	2120 ornithine carbamoyltransferase	16.14	down	0.00563
K02100_at	K02100	2123 angiotensinogen	10.24	down	0.00009
K02215_at	K02215	2124 coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B)	16.51	down	0.00006
K02402_at	K02402	2125 complement component 9	28.81	down	0.00001
K02766_at	K02766	2126 cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6	21.24	down	0
K03192_f_at	K03192	2127 cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6	69.92	down	0
K03192_f_at	K03192	2127 antithrombin III	50.16	down	0
L00190_s_at	L00190	2130 low density lipoprotein receptor (familial cystathione-beta-synthase)	42.41	down	0.00012
L00352_at	L00352	2131 cytochrome P450, subfamily IVA, polypeptide 11	4.19	down	0.00352
L00972_at	L00972	2133 phosphoenolpyruvate carboxykinase 1 (soluble)	7.19	down	0.00008
L04751_at	L04751	2138 epoxide hydrolase 2, cytoplasmic	36.79	down	0.00004
L05144_at	L05144	2139 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutarylaciduria)	4.76	down	0.02289
L05779_at	L05779	2140 Coenzyme A dehydrogenase	5.35	down	0.00006
L07033_at	L07033	2144 carboxylesterase 1 (monocyte/macrophage	3.49	down	0
L07077_at	L07077	2145 carboxylesterase 1 (monocyte/macrophage	4.82	down	0.00403
L07765_at	L07765	2147	20.53	down	0.00025

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	P value
L07956_at	L07956	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, fatty-acid-Coenzyme A ligase, long-chain 1,fatty-acid-Coenzyme A ligase, long-chain 2 complement component 2)	5.6	down	0.00029
L09229_s_at	L09229	lysosomal-associated membrane protein 2 aldehyde oxidase 1	18.34	down	0.00016
L09708_at	L09708	complement component 4-binding protein, beta	3.92	down	0.000693
L09717_at	L09717	complement component 4-binding protein, beta	4.06	down	0.00034
L11005_at	L11005	complement component 4-binding protein, beta	16.3	down	0.00065
L11244_s_at	L11244	complement component 4-binding protein, beta	43.33	down	0_
L11244_s_at	L11244	hydroxysteroid (17-beta) dehydrogenase 2	12.03	down	0.0001
L11708_at	L11708	serine hydroxymethyltransferase 1 (soluble)	5.99	down	0.01516
L11931_at	L11931	phosphoenolpyruvate carboxykinase 1 (soluble)	7.27	down	0.00041
L12760_s_at	L12760	crystallin, zeta (quinone reductase)	12.75	down	0.00035
L13278_at	L13278	B-factor, proterdin	5.83	down	0.0034
L15702_at	L15702	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9	3.7	down	0.04693
L16883_s_at	L16883	gamma-glutamyl carboxylase	84.71	down	0.00327
L17128_at	L17128	phosphodiesterase 4A, cAMP-specific (Drosophila)-homolog phosphodiesterase E2)	4.02	down	0.00096
L20965_at	L20965	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	3.02	down	0.01177
L211893_at	L211893	collagen, type XVIII, alpha 1	13.18	down	0.00155
L22548_at	L22548	epoxide hydrolase 1, microsomal (xenobiotic)	3.87	down	0.0299
L25878_s_at	L25878	epoxide hydrolase 1, microsomal (xenobiotic)	26.84	down	0_
L25880_s_at	L25880	epoxide hydrolase 1, microsomal (xenobiotic)	58.7	down	0.00013
L27050_at	L27050	apolipoprotein F	10.26	down	0.00026
L29008_at	L29008	sorbitol dehydrogenase	3.51	down	0.00825
L29433_at	L29433	coagulation factor X	7.74	down	0.00244
L32140_at	L32140	afamin	17.31	down	0.00003
L32179_at	L32179	aryacetamide deacetylase (esterase)	23.83	down	0_
L34081_at	L34081	bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choloyltransferase)	11.96	down	0.00008

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
L35546_at	L35546	glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)	14.18	down	0.000018
L35546_at	L35546	glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)	2203	down	0.0005
L36033_at	L36033	stromal cell-derived factor 1	5.56	down	0.00603
L38490_s_at	L38490	ADP-ribosylation factor 4-like	5.1	down	0.01306
L38928_at	L38928	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	3.13	down	0.0267
L38928_at	L38928	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	10.97	down	0.0267
L40401_at	L40401	putative protein	5.17	down	0.00726
L40401_at	L40401	putative protein	6.97	down	0.00079
L40401_at	L40401	putative protein	4.26	down	0.00194
L41067_at	L41067	nuclear factor of activated T-cells, cytoplasmic 3	4.96	down	0.00473
L47726_at	L47726	phenylalanine hydroxylase	25.63	down	0.00019
L48516_at	L48516	paraoxonase 3	22.21	down	0.00004
L49169_at	L49169	FBJ murine osteosarcoma viral oncogene	3.4	down	0.01193
L76465_at	L76465	hydroxyprostaglandin dehydrogenase 15-(NAD)	3.56	down	0.00688
L76571_at	L76571	nuclear receptor subfamily 0, group B, member 2	4.44	down	0.00312
L76687_at	L76687	growth factor receptor-bound protein 14	5.16	down	0.00199
L76927_mai1_at	L76927	galactokinase 1	3.66	down	0.00999
L77567_s_at	L77567	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	3.14	down	0.04095
M10058_at	M10058	asialoglycoprotein receptor 1	23.96	down	0
M10612_at	M10612	apolipoprotein C-II	17.13	down	0.00746
M10942_at	M10942	metallothionein 1E (functional)	6.19	down	0.00428
M10943_at	M10943	metallothionein 1F (functional)	3.88	down	0
M11025_s_at	M11025	asialoglycoprotein receptor 2	17.56	down	0.00003
M11313_s_at	M11313	alpha-2-macroglobulin	10.05	down	0.00014
M11321_at	M11321	group-specific component (vitamin D binding	16.52	down	0.01416
M11437_at	M11437	kininogen	18.38	down	0.00006
M11437_cds1_at	M11437	kininogen	16.19	down	0.02277
M11437_cds2_at	M11437				

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
M11567_mra1_at	M11567	2239	angiogenin, ribonuclease, RNase A family, 5	32.25	down	0.0001
M12174_at	M12174	2242	ras homolog gene family, member B	5.44	down	0.0088
M12272_s_at	M12272	2243	alcohol dehydrogenase 1 (class I), alpha polypeptide, alcohol dehydrogenase 2 (class I), beta polypeptide, alcohol dehydrogenase 3 (class I)	32.42	down	0.0034
M12529_at	M12529	2244	apolipoprotein E	3.05	down	0.03776
M12625_at	M12625	2245	lechithin-cholesterol acyltransferase	4.55	down	0.01584
M12712_s_at	M12712	2246	protein C (inactivator of coagulation factors Va and VIIIa)	7.37	down	0.01866
M12963_s_at	M12963	2248	beta polypeptide, alcohol dehydrogenase 2 (class I), beta polypeptide, alcohol dehydrogenase 3 (class I)	48.95	down	0.00104
M13143_at	M13143	2249	kallikrein B plasma, (Fletcher factor) 1	10.39	down	0.00019
M13149_at	M13149	2250	histidine-rich glycoprotein	18.65	down	0.02974
M13232_s_at	M13232	2251	coagulation factor VII (serum prothrombin)	5.9	down	0.00014
M13690_s_at	M13690	2252	complement component 1 Inhibitor (angioedema, ceruloplasmin (ferroxidase))	6.07	down	0.00045
M13699_at	M13699	2253	ceruloplasmin (ferroxidase)	15.85	down	0.00012
M13829_s_at	M13829	2254	v-raf murine sarcoma 3611 viral oncogene	6.52	down	0
M14058_at	M14058	2256	complement component 1, r subcomponent	6.66	down	0.00229
M14091_at	M14091	2257	thyroxin-binding globulin	10.86	down	0.00024
M14218_at	M14218	2259	argininosuccinate lyase	9.03	down	0.00078
M14338_at	M14338	2260	protein S (alpha)	12.33	down	0
M14636_at	M14636	2262	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	3.45	down	0.00133
M15465_s_at	M15465	2266	pyruvate kinase, liver and RBC	6.1	down	0.00069
M15517_cds5_at	M15517	2267	EST	22.76	down	0.03365
M15656_at	M15656	2268	aldolase B, fructose-bisphosphate	96.66	down	0
M16447_at	M16447	2270	quinoid dihydropteridine reductase	6.57	down	0.00015
M16474_s_at	M16474	2271	butyrylcholinesterase	5.82	down	0.00113
M16594_at	M16594	2272	glutathione S-transferase A2	73.21	down	0
M16750_s_at	M16750	2273	pim-1 oncogene	3.08	down	0.01811
M16961_at	M16961	2274	alpha-2-HS-glycoprotein	21.45	down	0.01175

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
M16967_at	M16967	2275	coagulation factor V (proaccelerin, labile factor)	5.56	down	0.00047
M16973_at	M16973	2276	complement component 8, beta polypeptide	22.75	down	0.00001
M16974_s_at	M16974	2277	complement component 8, alpha polypeptide	49.47	down	0.00046
M17262_at	M17262	2278	coagulation factor II (thrombin)	44.3	down	0.00345
M17262_at	M17262	2278	coagulation factor II (thrombin)	14.24	down	0.00028
M17466_at	M17466	2279	coagulation factor XII (Hageman factor)	9.76	down	0.00285
M18533_at	M18533	2284	dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269,	3.45	down	0.00313
M19828_s_at	M19828	2287	apolipoprotein B (including Ag(x) antigen)	29.37	down	0.00137
M20218_at	M20218	2288	coagulation factor XI (plasma thromboplastin	6.4	down	0.00004
M20786_at	M20786	2290	alpha-2-plasmin inhibitor	16.95	down	0.00709
M20867_s_at	M20867	2291	glutamate dehydrogenase 1	17.73	down	0.00002
M20902_at	M20902	2292	apolipoprotein C-I	3.14	down	0.0389
M21642_at	M21642	2294	antithrombin III	15.82	down	0.01027
M21642_s_at	M21642	2294	antithrombin III	15.23	down	0.02088
M22976_at	M22976	2297	cyclochrome b-5	7.39	down	0.02431
M23161_at	M23161	2298	EST	3.44	down	0.00733
M23234_s_at	M23234	2299	ATP-binding cassette, sub-family B (MDR/TAP), androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	10.05	down	0
M23263_at	M23263	2300	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	4.6	down	0.00005
M23263_at	M23263	2300	testicular adhesion molecule 1 (CD54), human	3.35	down	0.02551
M24283_at	M24283	2303	rhinovirus receptor	3.19	down	0.04985
M25079_s_at	M25079	2305	hemoglobin, beta	9.15	down	0.01399
M25280_at	M25280	2306	selectin L (lymphocyte adhesion molecule 1)	3.39	down	0.004
M26393_s_at	M26393	2309	acyl-Coenzyme A dehydrogenase, C-2 to C-3	16.27	down	0.00007
M27492_at	M27492	2312	interleukin 1 receptor, type I	4.62	down	0.0082

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
M29194_at	M29194	2315	lipase, hepatic	12.18	down	0.00012
M29873_s_at	M29873	2318	cytochrome P450, subfamily IIB (phenobarbital-	56.71	down	0.0054
M29874_s_at	M29874	2319	cytochrome P450, subfamily IIB (phenobarbital-	18.44	down	0.00081
M29971_at	M29971	2320	O-6-methylguanine-DNA methyltransferase	3.97	down	0.00424
M30185_at	M30185	2321	cholesteryl ester transfer protein, plasma	3.83	down	0.0013
M30185_at	M30185	2321	cholesteryl ester transfer protein, plasma	3.39	down	0.00089
M30257_s_at	M30257	2322	vascular cell adhesion molecule 1	3.11	down	0.00064
M30269_at	M30269	2323	nidogen (enactin)	3.4	down	0.00026
M31169_s_at	M31169	2325	propionyl Coenzyme A carboxylase, beta	4.65	down	0.00467
M31627_at	M31627	2330	X-box binding protein 1	6.97	down	0.00052
M31667_f_at	M31667	2331	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2	4.38	down	0.00078
M31994_at	M31994	2332	aldehyde dehydrogenase 1, soluble	11.24	down	0.01192
M333317_f_at	M333317	2338	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7	32.63	down	0
M333318_f_at	M333318	2339	cytochrome P450, subfamily I (phenobarbital-inducible), polypeptide 6	3.21	down	0.01621
M34276_at	M34276	2341	plasminogen	24.73	down	0.00031
M35410_s_at	M35410	2344	insulin-like growth factor binding protein 2 (36kD)	6.45	down	0.04517
MIP1-B_at	M35590	2345	small inducible cytokine A4	5.96	down	0.00604
MIP1-B_at	M35590	2345	small inducible cytokine A4	4.74	down	0.01225
MIP1-B_at	M35590	2345	small inducible cytokine A4	4.62	down	0.01268
M35878_at	M35878	2346	insulin-like growth factor binding protein 3	4.3	down	0.0027
M37400_at	M37400	2348	glutamic-oxaloacetic transaminase 1, soluble aspartate aminotransferase 1)	8.7	down	0.0004
M55150_at	M55150	2352	fumarylacetoacetate	3.93	down	0.00213
M55513_s_at	M55513	2354	potassium voltage-gated channel, shaker-related subfamily, member 5	4.81	down	0.02141
M55671_at	M55671	2355	protein Z, vitamin K-dependent plasma	4.74	down	0.00078
M57731_s_at	M57731	2359	GRO2 oncogene	13.87	down	0.0123
M58286_s_at	M58286	2360	tumor necrosis factor receptor superfamily,	8.15	down	0.00037

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
M58569_s_at	M58569	2361	EST	16.15	down	0.00174
M58600_ma1_at	M58600	2362	heparin cofactor II tissue factor pathway inhibitor (lipoprotein-)	39.79	down	0.00034
M59499_at	M59499	2363	associated coagulation inhibitor	5.92	down	0.0005
M59815_at	M59815	2364	complement component 4A sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	8.02	down	0.00049
M59916_at	M59916	2365	growth arrest and DNA-damage-inducible, alpha cytochrome P450, subfamily IIIC (mephenytoin 4-hydroxylase), polypeptide 18	3.36	down	0.0038
M60974_s_at	M60974	2368	cytochrome P450, subfamily IIIC (mephenytoin 4-hydroxylase), polypeptide 18	3.48	down	0.00209
M61853_at	M61853	2369	cytochrome P450, subfamily IIIC (mephenytoin 4-hydroxylase), polypeptide 18	7.82	down	0.00024
M61854_s_at	M61854	2370	cytochrome P450, subfamily IIIC (mephenytoin 4-hydroxylase), polypeptide 18	3.3	down	0.04185
M61855_at	M61855	2371	insulin-like growth factor-binding protein 4 complement component 4-binding protein 4	38.82	down	0.00023
M62403_s_at	M62403	2373	insulin-like growth factor-binding protein 4 complement component 4-binding protein 4	4.12	down	0.00226
M62486_at	M62486	2374	glutathione S-transferase M1,glutathione S-transferase M2 (muscle)glutathione S-aldehyde dehydrogenase 5	22.08	down	0.00272
M63509_s_at	M63509	2376	aldehyde dehydrogenase 5	7.06	down	0.03887
M63967_at	M63967	2378	coagulation factor XIII, B polypeptide glycine decarboxylase (decarboxylating, glycine decarboxylase, glycine cleavage system protein methylmalonyl Coenzyme A mutase)	4.04	down	0.00058
M64554_ma1_at	M64554	2380	H factor (complement)-like 1,H factor 1 protein C inhibitor (plasminogen activator inhibitor monoamine oxidase A alcohol dehydrogenase 6 (class V))	5.87	down	0.00011
M64590_at	M64590	2381	monoamine oxidase B	6.41	down	0.00002
M65131_ma1_at	M65131	2384	methymalonyl Coenzyme A mutase	7.44	down	0.00004
M65134_s_at	M65134	2385	complement component 5	12.01	down	0.00012
M65292_s_at	M65292	2386	H factor (complement)-like 1,H factor 1 protein C inhibitor (plasminogen activator inhibitor monoamine oxidase A alcohol dehydrogenase 6 (class V))	7.56	down	0.01152
M68316_ma1_at	M68316	2387	monoamine oxidase B	20.54	down	0
M68840_at	M68840	2388	monoamine oxidase A	3.96	down	0.01396
M68895_ma1_at	M68895	2390	alcohol dehydrogenase 6 (class V)	4.25	down	0.00354
M69177_at	M69177	2392	monoamine oxidase B	11.64	down	0.00001
M72885_ma1_s_at	M72885	2393	putative lymphocyte G0/G1 switch gene	6.5	down	0.03461
M74587_ma1_s_at	M74587	2394	insulin-like growth factor binding protein 1 carboxypeptidase B2 (plasma)	11.42	down	0.00274
M75106_at	M75106	2397	carboxypeptidase B2 (plasma)	40.63	down	0

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
M76665_at	M76665	2398	hydroxysteroid (11-beta) dehydrogenase 1	19.22	down	0.000044
M80482_at	M80482	2403	paired basic amino acid cleaving system 4	4.26	down	0.00041
M81182_s_at	M81182	2404	ATP-binding cassette, sub-family D (ALD),	3.45	down	0.00499
M81349_at	M81349	2405	serum amyloid A4, constitutive	76.15	down	0.00015
M83216_s_at	M83216	2407	caldesmon 1	4.27	down	0.00037
M83652_s_at	M83652	2408	properdin P factor, complement	6	down	0.00002
M83772_at	M83772	2409	flavin containing monooxygenase 3	19.54	down	0
M86826_at	M86826	2413	insulin-like growth factor binding protein, acid	3.75	down	0.01157
M86873_s_at	M86873	2414	plasminogen,plasminogen-like	17.54	down	0
M88163_at	M88163	2416	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	3.37	down	0.00098
M91432_at	M91432	2420	acyl-Coenzyme A dehydrogenase, C-4 to C-12	6.74	down	0.00008
M92843_s_at	M92843	2421	zinc finger protein homologous to Zfp-36 ln	3.02	down	0.04958
M93143_at	M93143	2423	plasminogen-like	10.06	down	0.00098
M93405_at	M93405	2424	methylmalonate-semialdehyde dehydrogenase	23.06	down	0
M94065_at	M94065	2425	dihydroorotate dehydrogenase	11.78	down	0.00034
M94065_at	M94065	2425	dihydroorotate dehydrogenase	6.47	down	0.00013
M95585_s_at	M95585	2430	hepatic leukemia factor	4.2	down	0.00212
M95767_at	M95767	2432	chitobiase, di-N-acetyl-glutathione S-transferase, di-N-acetyl-glutathione S-transferase M1,glutathione S-	4.94	down	0.00004
M96233_s_at	M96233	2433	transferase M2 (muscle),glutathione S-	4.23	down	0.04227
M96843_at	M96843	2435	EST	8.42	down	0.02394
M96843_at	M96843	2435	EST	4.08	down	0.02912
M99439_at	M99439	2438	transducin-like enhancer of split 4, homolog of	5.14	down	0.00001
rc_N20113_s_at	N20113	2439	EST	5.24	down	0.01346
rc_N21079_at	N21079	2441	nucleolar cysteine-rich protein	4.1	down	0.00028
rc_N21550_at	N21550	2444	EST	3.08	down	0.00006
rc_N21646_at	N21646	2446	EST	3.79	down	0.00079
rc_N22404_at	N22404	2450	EST	3.99	down	0.01152
rc_N22434_at	N22434	2451	EST	4.37	down	0.01725
rc_N22854_s_at	N22854	2452	CASP2 and RIPK1 domain containing adaptor	3.34	down	0.0084

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_N22938_s_at	N22938	2453	serum amyloid A4, constitutive	35.39	down	0.00128
rc_N23665_s_at	N23665	2455	hydroxysteroid (17-beta) dehydrogenase 2	9.4	down	0.00055
rc_N23730_s_at	N23730	2456	v-fos FBJ murine osteosarcoma viral oncogene	4.38	down	0.04395
rc_N23761_at	N23761	2457	DKFZP586G011 protein	5.41	down	0.00448
N23817_at	N23817	2458	EST	3.76	down	0.00288
rc_N24879_at	N24879	2460	EST	9.44	down	0.00008
rc_N25082_s_at	N25082	2463	amplified in osteosarcoma	5.19	down	0.00895
rc_N25193_at	N25193	2464	EST	3.13	down	0.01955
protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	2466			4.32	down	0.00304
rc_N25969_s_at	N25969			4.82	down	0.00056
rc_N26184_at	N26184	2467	MYLE protein	3.13	down	0.00216
rc_N27524_at	N27524	2472	EST	3.3	down	0.00021
rc_N27563_at	N27563	2473	EST	6.15	down	0.00321
N27670_at	N27670	2474	progesterone membrane binding protein	5.31	down	0.00039
rc_N27834_at	N27834	2475	alpha2,3-sialyltransferase	4.58	down	0.00011
rc_N29319_at	N29319	2476	EST	4.78	down	0.00019
rc_N29353_at	N29353	2477	kynureine 3-monooxygenase (kynureine 3-solute carrier family 19 (thiamine transporter),	3.71	down	0.00393
rc_N30856_at	N30856	2485	2485	3.1	down	0.00203
rc_N31598_at	N31598	2488	EST	14.76	down	0.00001
rc_N31741_at	N31741	2489	serine hydroxymethyltransferase 1 (soluble)	3.13	down	0.01481
rc_N31952_at	N31952	2490	EST	8.75	down	0.00006
rc_N32071_at	N32071	2491	EST	60.54	down	0.0093
rc_N33009_s_at	N33009	2492	apolipoprotein E	3.07	down	0.00186
rc_N34441_at	N34441	2496	EST	4.3	down	0.00028
rc_N34804_at	N34804	2497	DKFZP434J214 protein	6.16	down	0.00222
rc_N36001_at	N36001	2504	EST	4.06	down	0.00776
rc_N36250_at	N36250	2506	cellular repressor of E1A-stimulated genes	4.3	down	0.03917
rc_N39163_at	N39163	2509	metallothionein 1L	24.91	down	0.00253
rc_N39201_at	N39201	2510	protease inhibitor 4 (kallistatin)	3.72	down	0.01771
rc_N40188_at	N40188	2513	EST	7.56	down	0.01584
N40320_at	N40320	2514	EST			

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_N45232_at	N45232	2517	EST	3.61	down	0.01308
rc_N45307_s_at	N45307	2518	EST	4.55	down	0.00006
rc_N45998_at	N45998	2520	EST	3.14	down	0.00337
rc_N47469_at	N47469	2522	EST	3.34	down	0.00329
rc_N47942_at	N47942	2523	progesterone membrane binding protein	4.51	down	0.00168
rc_N48180_at	N48180	2526	EST	3.36	down	0.00543
rc_N48315_at	N48315	2527	adaptor-related protein complex 2, mu 1 subunit	5.3	down	0.0149
rc_N48602_at	N48602	2529	EST	3.17	down	0.02913
rc_N48674_at	N48674	2530	EST	4.06	down	0.00028
rc_N48787_at	N48787	2531	protease inhibitor 1 (anti-elastase), alpha-1-	4.4	down	0.00292
rc_N49090_at	N49090	2533	EST	18	down	0.00501
rc_N49104_s_at	N49104	2534	nuclear receptor interacting protein 1	3.83	down	0.00144
rc_N49113_at	N49113	2535	EST	3.4	down	0.00162
rc_N49214_at	N49214	2536	EST	4.74	down	0.00064
rc_N49595_at	N49595	2538	EST	10.39	down	0.00022
rc_N49902_at	N49902	2540	EST	3.55	down	0.00455
rc_N51117_at	N51117	2544	EST	9.68	down	0.00081
rc_N51737_at	N51737	2547	mitogen-activated protein kinase kinase	3.32	down	0.00376
rc_N51773_at	N51773	2549	EST	16.32	down	0.0007
rc_N52271_at	N52271	2552	LIM protein (similar to rat protein kinase C-	8.06	down	0.00011
rc_N52322_at	N52322	2553	EST	3.27	down	0.00933
rc_N52845_at	N52845	2554	EST	5.53	down	0.00088
rc_N52985_at	N52985	2555	nidogen (enactin)	4.21	down	0.01385
rc_N53031_s_at	N53031	2556	UDP glycosyltransferase 2 family, polypeptide B4	97.58	down	0.00022
rc_N53352_at	N53352	2558	EST	3.22	down	0.00416
rc_N53549_s_at	N53549	2559	cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase) polypeptide 2	4.68	down	0.00818
rc_N53757_at	N53757	2560	EST	3.97	down	0.00255
rc_N54053_at	N54053	2561	secreted phosphoprotein 2, 24kD	60.39	down	0.00087
rc_N54311_at	N54311	2564	EST	4.82	down	0.00183
rc_N54399_at	N54399	2566	EST	3.34	down	0.00048

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_N54417_s_at	N54417	2567	fibrinogen, A alpha polypeptide	99.28	down	0.00001
rc_N54429_at	N54429	2568	EST	57.81	down	0.00724
rc_N54511_s_at	N54511	2569	KIAA0265 protein	3.45	down	0.03362
rc_N54604_at	N54604	2570	EST	3.72	down	0.00741
rc_N54792_at	N54792	2571	cytidine monophosphate-N-acetylneuraminate hydroxylase (CMP-N-acetylneuraminate)	3.23	down	0.00099
rc_N54950_s_at	N54950	2573	ketohexokinase (fructokinase)	17.17	down	0.00078
rc_N57464_at	N57464	2576	CCAAT/enhancer binding protein (C/EBP), delta	14.69	down	0.00018
rc_N57934_s_at	N57934	2577	formiminotransferase cyclodeaminase	13.81	down	0.00171
rc_N58326_at	N58326	2579	EST	14.97	down	0.00647
rc_N59089_at	N59089	2581	EST	4.74	down	0.00055
rc_N59231_s_at	N59231	2582	pyruvate carboxylase	3.45	down	0.02066
rc_N59283_at	N59283	2583	EST	4.65	down	0.02343
rc_N59474_at	N59474	2584	EST	6.93	down	0.00337
rc_N59532_s_at	N59532	2585	aminomethyltransferase (glycine cleavage	6.73	down	0.00005
rc_N59543_at	N59543	2587	PDZ domain containing 1	9.96	down	0.00052
rc_N59550_at	N59550	2588	EST	25.56	down	0.00024
rc_N62443_at	N62443	2590	EST	3.72	down	0.01717
rc_N62523_at	N62523	2592	hepatocarcinoma factor	5.02	down	0.00087
rc_N62652_s_at	N62652	2593	EST	5.23	down	0.03006
rc_N63391_at	N63391	2600	EST	7.39	down	0.00565
rc_N63688_at	N63688	2603	EST	3.13	down	0.002
rc_N63698_at	N63698	2604	EST	7.92	down	0.00001
rc_N63845_at	N63845	2605	phytanoyl-CoA hydroxylase (Refsum disease)	25.92	down	0.00084
rc_N64017_at	N64017	2606	EST	5.27	down	0.00022
rc_N64036_s_at	N64036	2607	Coenzyme A, hydratase/3-hydroxyacyl	9.99	down	0.00125
rc_N64436_at	N64436	2609	EST	3.51	down	0.00441
rc_N64535_at	N64535	2610	EST	6.19	down	0.00106
rc_N65959_at	N65959	2612	EST	5.43	down	0.00044
rc_N66066_at	N66066	2613	EST	28.35	down	0.00055

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_N66130_at	N66130	2614	progesterone membrane binding protein	3.98	down	0.0106
rc_N66422_at	N66422	2616	EST	4.1	down	0.00237
rc_N66763_at	N66763	2619	EST	3.79	down	0.03015
rc_N66857_at	N66857	2620	EST	15.03	down	0.000005
rc_N67009_s_at	N67009	2622	Gerstmann-Straussler-Scheinker syndrome, fatal	3.55	down	0.00956
rc_N67096_at	N67096	2623	EST	3.23	down	0.00446
rc_N67105_at	N67105	2624	EST	5.01	down	0.00176
rc_N67378_at	N67378	2626	KIAA1053 protein	7.14	down	0
rc_N67876_s_at	N67876	2628	insulin-like growth factor 1 (somatomedin C)	8.89	down	0.00042
rc_N67893_at	N67893	2629	EST	10.48	down	0.00341
rc_N68596_s_at	N68596	2636	betaine-homocysteine methyltransferase	40.99	down	0
rc_N68730_at	N68730	2637	EST	3.88	down	0.00091
rc_N68974_at	N68974	2640	EST	16.44	down	0.00087
rc_N68993_at	N68993	2641	EST	3.06	down	0.00867
rc_N69136_at	N69136	2645	EST	18.53	down	0.00366
rc_N69216_at	N69216	2646	EST	3.4	down	0.00497
rc_N69299_at	N69299	2649	EST	3.63	down	0.03776
rc_N70005_at	N70005	2653	EST	3.42	down	0.04229
rc_N70057_s_at	N70057	2654	DNA segment on chromosome 6 (unique) 49	5.24	down	0.01178
rc_N70305_at	N70305	2655	EST	4.41	down	0.00078
rc_N70358_s_at	N70358	2657	growth hormone receptor	34.35	down	0
rc_N70861_at	N70861	2661	EST	6.55	down	0.00001
rc_N70966_s_at	N70966	2663	cotransporter family), member 1	34.06	down	0.0006
rc_N71542_at	N71542	2665	kidney- and liver-specific gene	21.05	down	0
rc_n71935_s_at	N71935	2667	multiple PDZ-domain protein	16.28	down	0
rc_N72259_at	N72259	2670	connexin-like	4.65	down	0.0054
rc_N72695_s_at	N72695	2671	EST	9.18	down	0.00069
rc_N73461_f_at	N73461	2673	EST	4.25	down	0.00162
rc_N73468_s_at	N73468	2674	protein S (alpha)	4.4	down	0.00853

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
rc_N73543_at	N73543	2675	EST	17	down	0.00003
rc_N73561_at	N73561	2676	EST	12.96	down	0.00011
rc_N73883_at	N73883	2682	EST	9.35	down	0
rc_N73988_at	N73988	2683	EST	10.27	down	0.00083
rc_N74025_at	N74025	2685	deiodinase, iodothyronine, type I	22.79	down	0
rc_N74422_at	N74422	2686	EST	30.32	down	0.00247
rc_N74558_at	N74558	2687	EST	3.19	down	0.00379
rc_N75072_at	N75072	2689	EST	3.73	down	0.00181
N75203_s_at	N75203	2691	EST	6.15	down	0.00251
N75870_s_at	N75870	2693	dual specificity phosphatase 1	13.41	down	0.00598
rc_N76012_r_at	N76012	2694	EST	36.71	down	0.00542
N77326_at	N77326	2696	EST	7.51	down	0.00119
N77606_at	N77606	2697	EST	4.22	down	0.00421
rc_N78850_s_at	N78850	2699	macrophage stimulating 1 (hepatocyte growth factor-like), macrophage stimulating, pseudogene	13.69	down	0.00421
rc_N78902_at	N78902	2700	lepin receptor	6.79	down	0.0041
rc_N79435_at	N79435	2701	chromosome 15 open reading frame 3	3.12	down	0.00861
rc_N79778_at	N79778	2702	extracellular matrix protein 2, female organ and	5.15	down	0.00286
rc_N80129_1_at	N80129	2703	metallothionein 1L	66.48	down	0.00415
rc_N80129_f_at	N80129	2703	metallothionein 1L	13.6	down	0.00196
rc_N81025_at	N81025	2705	EST	8.61	down	0.00015
rc_N81036_at	N81036	2706	EST	6.89	down	0.00276
N89302_s_at	N89302	2708	HLA-B associated transcript-3	23.44	down	0.00192
rc_N89738_at	N89738	2710	EST	10.06	down	0.00052
rc_N90584_at	N90584	2714	EST	3.08	down	0.02602
N90820_at	N90820	2715	DKFZP566B1346 protein	4.86	down	0.03008
N91087_at	N91087	2717	EST	6.91	down	0.00109
rc_N91273_1_at	N91273	2718	EST	4.07	down	0.02965
rc_N91882_at	N91882	2720	alpha2,3-sialyltransferase	14.52	down	0.00024
rc_N93155_f_at	N93155	2729	calmodulin 1 (phosphorylase kinase, delta)	4.39	down	0.0002
rc_N93155_1_at	N93155	2729	calmodulin 1 (phosphorylase kinase, delta)	3.46	down	0.00031

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_N93191_at	N93191	2730	EST	3.25	down	0.000232
rc_N93246_f_at	N93246	2731	EST	3.03	down	0.00049
rc_N93764_at	N93764	2737	EST	5.92	down	0.0109
N94146_at	N94146	2739	EST	8.05	down	0
rc_N94367_at	N94367	2740	EST	8.79	down	0.01003
rc_N94930_at	N94930	2741	multiple PDZ domain protein	10.06	down	0.00226
rc_N95495_at	N95495	2742	EST	5.61	down	0.00308
rc_N95585_at	N95585	2743	EST	3.1	down	0.0083
N99542_at	N99542	2747	orosomucoid 1	8.41	down	0.00001
rc_N99866_at	N99866	2748	EST	3.13	down	0.04148
rc_R00296_at	R00296	2750	EST	3.98	down	0.04632
rc_R00843_s_at	R00843	2751	fragile histidine triad gene	3.68	down	0.03578
rc_R01023_s_at	R01023	2752	glucokinase (hexokinase 4) regulatory protein	50.71	down	0.00321
rc_R01081_at	R01081	2753	EST	3.3	down	0.00839
rc_R02365_f_at	R02365	2755	storage disease type I, von Gierke disease)	17.17	down	0.00124
rc_R02371_at	R02371	2756	EST	3.75	down	0.00009
rc_R02572_at	R02572	2757	fibronectin 1	7.1	down	0.00059
rc_R02752_at	R02752	2758	EST	3.05	down	0.00362
rc_R05309_f_at	R05309	2759	EST	3.72	down	0.0008
rc_R05490_at	R05490	2761	SEC24 (S. cerevisiae) related gene family,	3.03	down	0.00317
rc_R05518_at	R05518	2762	EST	4.15	down	0.0125
rc_R06002_s_at	R06002	2763	EST	10.15	down	0.00003
rc_R06271_s_at	R06271	2766	EST	6.14	down	0.00063
rc_R06726_s_at	R06726	2770	protease inhibitor 1 (anti-elastase), alpha-1-	12.26	down	0.03905
rc_R06746_at	R06746	2771	EST	15.77	down	0.00009
rc_R06764_s_at	R06764	2772	apolipoprotein B (including Ag(x) antigen)	4.91	down	0.00167
rc_R06977_f_at	R06977	2775	glucokinase (hexokinase 4) regulatory protein	6.1	down	0.00049
rc_R07637_at	R07637	2778	EST	3.04	down	0.00118
rc_R08548_at	R08548	2779	EST	9.94	down	0.00326
rc_R08564_at	R08564	2780	plasminogen-like	60.18	down	0.00091

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_R08615_s_at	R08615	2781	homogenisate 1,2-dioxygenase (homogenisate)	21.85	down	0.00026
rc_R08850_s_at	R08850	2782	EST	12.55	down	0.00009
rc_R09053_at	R09053	2783	EST	5.9	down	0.0002
rc_R10138_at	R10138	2784	EST	4	down	0.00032
rc_R10287_at	R10287	2785	EST	11.2	down	0.0003
rc_R10378_s_at	R10378	2786	fibrinogen-like 1	8.13	down	0.00189
rc_R10662_f_at	R10662	2787	mult (E. coli) homolog 1 (colon cancer,	3.2	down	0.0005
rc_R10684_at	R10684	2788	EST	5.51	down	0.00741
rc_R12472_at	R12472	2789	EST	55.18	down	0.00011
rc_R12579_at	R12579	2790	EST	3.5	down	0.00137
rc_R15825_f_at	R15825	2792	KIAA0946 protein; Huntingtin interacting protein	5.33	down	0.00391
rc_R16098_at	R16098	2793	EST	63.41	down	0.00038
rc_R17762_at	R17762	2795	EST	3.37	down	0.01822
rc_R21232_at	R21232	2798	EST	3.56	down	0.00246
rc_R22196_at	R22196	2799	EST	3.75	down	0.02867
rc_R22905_at	R22905	2801	EST	4.64	down	0.0043
rc_R26904_f_at	R26904	2805	EST	3.51	down	0.00058
rc_R31641_at	R31641	2814	EST	9.96	down	0.00011
rc_R31917_s_at	R31917	2815	EST	3.91	down	0.00071
rc_R32036_s_at	R32036	2816	Interleukin 1 receptor-like 1	4.02	down	0.00051
rc_R32440_at	R32440	2817	EST	7.41	down	0.00159
rc_R32490_s_at	R32490	2818	EST	8.95	down	0.00215
rc_R33146_at	R33146	2819	EST	7	down	0.00043
rc_R34133_at	R34133	2821	EST	4.13	down	0.00008
rc_R34362_at	R34362	2822	KIAA0327 gene product	5.4	down	0.04615
rc_R36228_at	R36228	2824	EST	4.39	down	0.00033
rc_R36989_s_at	R36989	2826	hypothetical protein, estradiol-induced	13.7	down	0.00056
rc_R37128_s_at	R37128	2827	complement component 4A	39.51	down	0.00364
rc_R38185_at	R38185	2829	EST	6.32	down	0.00063
rc_R38709_s_at	R38709	2833	superoxide dismutase 2, mitochondrial	8.23	down	0.01578
rc_R39234_f_at	R39234	2835	EST	3.24	down	0.0412

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_R40395_s_at	R40395	2841	lecithin-cholesterol acyltransferase	37.33	down	0.00032
rc_R40492_at	R40492	2842	EST	8.89	down	0.00229
rc_R40556_s_at	R40556	2843	EST	3.57	down	0.00184
rc_R40899_f_at	R40899	2844	glycine receptor, beta	9.11	down	0.0009
rc_R40946_f_at	R40946	2845	crystallin, zeta (quinone reductase)	6.14	down	0.00156
rc_R42241_at	R42241	2846	EST	3.97	down	0.00129
rc_R43166_l_at	R43166	2847	EST	3.37	down	0.00919
rc_R43174_s_at	R43174	2848	paraoxonase 1	74.04	down	0.00038
rc_R43365_at	R43365	2850	EST	5.37	down	0.00103
rc_R43799_at	R43799	2851	EST	16.35	down	0.00208
rc_R43910_at	R43910	2852	EST	5.71	down	0
rc_R44025_at	R44025	2854	EST	4.4	down	0.01325
rc_R44761_at	R44761	2858	aryl hydrocarbon receptor nuclear translocator	3.12	down	0.02663
rc_R45656_j_at	R45656	2865	EST	10.21	down	0.00179
rc_R48307_at	R48307	2870	EST	7.18	down	0.00007
rc_R48540_s_at	R48540	2873	EST	6.05	down	0.00086
rc_R48732_s_at	R48732	2876	EST	5.12	down	0.00837
rc_R49035_at	R49035	2877	EST	8.02	down	0.00991
rc_R49459_s_at	R49459	2882	transferrin receptor 2	85.61	down	0.00048
rc_R49602_at	R49602	2885	EST	36.5	down	0.00001
rc_R50008_s_at	R50008	2887	7-dehydrocholesterol reductase	6.67	down	0.00409
rc_R51256_at	R51256	2889	EST	3.04	down	0.00286
rc_R51309_at	R51309	2890	KIAA1077 protein	3.54	down	0.04112
rc_R51831_at	R51831	2891	EST	5.03	down	0.00761
rc_R52800_at	R52800	2895	EST	3.96	down	0.00749
rc_R52822_l_at	R52822	2896	EST	12.79	down	0.00001
rc_R52949_at	R52949	2897	EST	3.46	down	0.00395
rc_R54416_at	R54416	2901	EST	3.14	down	0.00236
rc_R56094_at	R56094	2905	EST	4.87	down	0.00214
rc_R56602_at	R56602	2907	Ig superfamily protein	3.06	down	0.02464
rc_R59221_at	R59221	2912	progesterone binding protein	7.54	down	0.00159

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_R59325_at	R59325	2914	EST	4.48	down	0.00117
rc_R59722_at	R59722	2916	EST	19.74	down	0.00016
rc_R61740_f_at	R61740	2923	EST	4.02	down	0.00321
rc_R62173_f_at	R62173	2924	UDP-glucose dehydrogenase	5.76	down	0.0006
rc_R62519_f_at	R62519	2926	EST	10.83	down	0.00243
rc_R63545_at	R63545	2927	EST	5.4	down	0.00202
rc_R64131_at	R64131	2930	EST	20.58	down	0.01028
rc_R64144_s_at	R64144	2932	CAMP responsive element binding protein-like 2	4.58	down	0.00495
rc_R64199_at	R64199	2933	SEC22, vesicle trafficking protein (<i>S. cerevisiae</i>)-	9.19	down	0.00387
rc_R65593_s_at	R65593	2935	lumurenine 3-monoxygenase (kyurenine 3-	21.27	down	0.00007
rc_R67751_at	R67751	2939	EST	3.12	down	0.00319
rc_R67970_s_at	R67970	2940	gamma-glutamyl carboxylase	9.45	down	0.00212
rc_R69031_at	R69031	2941	EST	3.19	down	0.00798
rc_R69417_at	R69417	2942	EST	7.79	down	0.03795
rc_R70790_at	R70790	2948	EST	4.07	down	0.02354
rc_R71491_at	R71491	2954	EST	3.55	down	0.01903
rc_R73485_at	R73485	2958	EST	7.77	down	0.0009
rc_R73816_at	R73816	2961	EST	11.53	down	0.00259
R77628_at	R77628	2966	Insulin induced gene 1	29.23	down	0.00122
R80048_at	R80048	2972	EST	12.28	down	0.00128
R80573_at	R80573	2973	EST	3.08	down	0.02126
rc_R82074_f_at	R82074	2974	syndecan 1	6.66	down	0.01336
R82229_at	R82229	2975	phosphatidylserine decarboxylase	3.08	down	0.03455
rc_R82837_at	R82837	2976	KIAA0970 protein	5	down	0.00181
R87373_s_at	R87373	2978	EST	4.09	down	0.02253
rc_R89811_s_at	R89811	2980	HGF activator	62.51	down	0.00148
rc_R91503_s_at	R91503	2982	ATP-binding cassette, sub-family C (CFTR/MRP),	9.64	down	0.00584
rc_R92458_f_at	R92458	2986	hemoglobin, gamma G	3.31	down	0.000763
rc_R92475_s_at	R92475	2987	flavin containing monooxygenase 3	26.13	down	0
rc_R92737_at	R92737	2988	EST	4.53	down	0.04447
rc_R92768_at	R92768	2989	EST	13.2	down	0.00001

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_R93714_at	R93714	2992	fetuin B	10.42	down	0.00043
R93776_s_at	R93776	2993	EST	39.32	down	0.00176
rc_R93908_at	R93908	2994	EST	5.8	down	0.02699
R94662_at	R94662	2995	heme-binding protein	4.41	down	0.02301
rc_R94674_s_at	R94674	2996	EST	10.76	down	0.00008
R96417_at	R96417	2998	EST	3.9	down	0.00019
rc_R96822_at	R96822	3000	EST	8.25	down	0.00008
rc_R97302_at	R97302	3003	EST	3.73	down	0.01887
rc_R97419_at	R97419	3004	alpha-hydroxylase), polypeptide 1	65.07	down	0.0039
rc_R97711_at	R97711	3005	EST	3.37	down	0.00838
rc_R97798_at	R97798	3007	EST	3.79	down	0.00015
R98073_at	R98073	3009	EST	46.87	down	0
rc_R98074_at	R98074	3010	EST	9.21	down	0.00048
rc_R98413_at	R98413	3012	EST	9.71	down	0.00007
rc_R98624_at	R98624	3013	EST	21.32	down	0
rc_R98774_at	R98774	3014	EST	3.93	down	0.00001
rc_R99591_at	R99591	3016	CD5 antigen-like (scavenger receptor cysteine	9.52	down	0.00006
rc_R99909_at	R99909	3017	EST	4.27	down	0.00045
S48983_at	S48983	3018	serum amyloid A4, constitutive	23.04	down	0.00022
S52028_s_at	S52028	3019	cystathione (cystathione gamma-lyase)	3.21	down	0.00476
S62539_s_at	S62539	3022	insulin receptor substrate 1	3.7	down	0.01307
S67325_at	S67325	3024	propionyl Coenzyme A carboxylase, beta aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid	4.19	down	0.00151
S68287_at	S68287	3025	dehydrogenase, type I; dihydrodiol	24.11	down	0
S68805_at	S68805	3026	glycine amidinotransferase (L-arginine:glycine	18.19	down	0.00083
S69232_at	S69232	3027	electron-transferring-flavoprotein dehydrogenase	4.9	down	0.00017
S70004_at	S70004	3029	glycogen synthase 2 (liver)	9.96	down	0.00001
S72370_at	S72370	3030	pyruvate carboxylase	5.31	down	0.00075
S72370_at	S72370	3030	pyruvate carboxylase	4.54	down	0.00001

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	P value
S74728_at	S74728	3033 antiquitin 1	5.01	down	0.00008
S77356_at	S77356	3034 EST	5.83	down	0.00122
S77410_at	S77410	3035 angiotensin receptor 1	10.4	down	0
S90469_at	S90469	3040 P450 (cytochrome) oxidoreductase	4.32	down	0.0182
S95936_at	S95936	3041 transferrin	19.76	down	0.02009
rc_T03441_f_at	T03441	3044 cytochrome b-561	5.74	down	0.02781
rc_T03651_s_at	T03651	3047 tubulin, beta polypeptide	6.47	down	0.00843
T08879_at	T08879	3049 cathepsin F	5.29	down	0.0008
rc_T10108_s_at	T10108	3050 EST	3.85	down	0.01155
rc_t10264_s_at	T10264	3051 EST	3.84	down	0.00874
rc_T10322_at	T10322	3053 dihydropyrimidinase-like 2	4.23	down	0.01527
rc_T10822_at	T10822	3055 EST	3.16	down	0.00635
rc_T15482_f_at	T15482	3060 EST	5.04	down	0.00233
rc_T15674_f_at	T15674	3061 EST	4.12	down	0.02111
rc_T16175_s_at	T16175	3064 protein tyrosine phosphatase, non-receptor type	3.07	down	0.01007
rc_T16269_at	T16269	3067 EST	3.36	down	0.00282
rc_T16478_at	T16478	3070 EST	4	down	0.01041
rc_T16484_s_at	T16484	3071 EST	7.69	down	0.00805
rc_T17411_s_at	T17411	3078 transthyretin (prealbumin, amyloidosis type I)	13.49	down	0.00203
rc_T23430_at	T23430	3080 EST	3.12	down	0.00949
rc_T23680_at	T23680	3084 calcium channel, voltage-dependent, gamma	3.29	down	0.0003
rc_T23882_s_at	T23882	3085 kininogen	42.85	down	0.00641
rc_T23986_s_at	T23986	3086 hydroxyacyl glutathione hydrolase; glyoxalase 2	7.26	down	0.0062
rc_T24055_s_at	T24055	3087 ribosomal protein L26	3.9	down	0.00046
rc_T24106_at	T24106	3089 EST	12.13	down	0.01687
rc_T25506_at	T25506	3090 EST	4.51	down	0.00529
T30341_s_at	T30341	3101 EST	3.04	down	0.04567
rc_T33011_at	T33011	3104 EST	3.57	down	0.02486
T39897_s_at	T39897	3114 androgen induced protein	10	down	0.00466
rc_T40936_at	T40936	3118 EST	46.92	down	0.00056
rc_T40995_f_at	T40995	3119 alcohol dehydrogenase 3 (class I), gamma	13.25	down	0.01531

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Afy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_T41047_s_at	T41047	3120	EST	4.74	down	0.00015
rc_T41232_at	T41232	3122	EST	3.57	down	0.00846
rc_T46901_at	T46901	3123	EST	77.28	down	0.0006
rc_T47778_s_at	T47778	3127	fibrinogen, A alpha polypeptide	30	down	0.01401
rc_T48039_s_at	T48039	3129	protein C (inactivator of coagulation factors Va	84.39	down	0.00112
rc_T48075_f_at	T48075	3130	hemoglobin, alpha 1	32.56	down	0.00172
rc_T48278_at	T48278	3132	EST	15.04	down	0.04751
rc_T48980_s_at	T48980	3134	calmodulin 1 (phosphorylase kinase, delta)	4.2	down	0.0046
rc_T49061_at	T49061	3135	EST	3.06	down	0.00768
rc_T51150_at	T51150	3137	EST	10.52	down	0.00377
rc_T51617_at	T51617	3138	solute carrier family 22 (extraneuronal monoamine transporter), member 3	17.67	down	0.00018
rc_T51930_at	T51930	3139	EST	9.99	down	0.00066
rc_T52564_at	T52564	3141	EST	3.28	down	0.01506
rc_T52813_s_at	T52813	3142	putative lymphocyte G0/G1 switch gene	16.71	down	0.03897
rc_T54160_s_at	T54160	3145	EST	3.24	down	0.00168
rc_T55547_at	T55547	3148	EST	3.28	down	0.00047
rc_T56264_s_at	T56264	3149	apolipoprotein C-II	53.04	down	0.00938
rc_T56279_s_at	T56279	3150	H factor (complement)-like 3	28.39	down	0.00016
rc_T56281_f_at	T56281	3151	RNA helicase-related protein	32.34	down	0.00002
T57140_s_at	T57140	3152	paraoxonase 3	28.8	down	0
rc_T58032_s_at	T58032	3153	3-hydroxyanthranilate 3,4-dioxygenase	8.86	down	0.00023
rc_T58756_at	T58756	3156	EST	13.39	down	0.00013
rc_T58775_at	T58775	3157	small inducible cytokine subfamily A (Cys-Cys), carbamoyl-phosphate synthetase 1, mitochondrial	21.18	down	0.00006
rc_T59148_s_at	T59148	3158	carbamoyl-phosphate synthetase 1, mitochondrial	88.89	down	0
rc_T60407_at	T60407	3161	EST	6.6	down	0.00167
rc_T61256_s_at	T61256	3162	ketohexokinase (fructokinase)	13.59	down	0.000425
rc_T61373_s_at	T61373	3163	vitronectin (serum spreading factor, somatomedin B, complement S-protein)	44.9	down	0.03172
rc_T61389_f_at	T61389	3164	haptoglobin	18.95	down	0.04873
rc_T61649_f_at	T61649	3165	superoxide dismutase 2, mitochondrial	26.09	down	0.00734

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_T61801_s_at	T61801	3167	hemopexin	25.7	down	0.01362
rc_T63364_at	T63364	3170	ficolin (collagen/fibronogen domain-containing) 3	6.72	down	0.00383
rc_T63490_at	T63490	3171	EST	16.54	down	0
rc_T64575_s_at	T64575	3172	EST	10.46	down	0.00014
rc_T64887_f_at	T64887	3173	protein phosphatase 5, catalytic subunit	5.66	down	0.00349
rc_T65972_at	T65972	3177	EST	3.21	down	0.04847
rc_T66189_s_at	T66189	3178	glutaryl-Coenzyme A dehydrogenase	8.61	down	0.00003
rc_T67231_at	T67231	3181	succinate dehydrogenase complex, subunit D, integral membrane protein	7.04	down	0.03554
rc_T67705_s_at	T67705	3183	asialoglycoprotein receptor 2	31.6	down	0.00705
rc_T67931_at	T67931	3184	fibrinogen, B beta polypeptide	49.55	down	0
rc_T68083_at	T68083	3185	short-chain dehydrogenase/reductase 1	4.03	down	0.01593
rc_T68426_s_at	T68426	3186	CD81 antigen (target of antiproliferative antibody	3.11	down	0.01634
rc_T68510_at	T68510	3187	EST	3.87	down	0.00617
rc_T68711_at	T68711	3188	EST	37.65	down	0.00036
rc_T68855_at	T68855	3189	EST	34.04	down	0
rc_T68873_f_at	T68873	3190	metallothionein 1L	28.72	down	0.02953
rc_T68878_f_at	T68878	3191	carboxylesterase 1 (monocyte/macrophage	60.35	down	0.00409
rc_T69009_s_at	T69009	3192	quinoid dihydropteridine reductase	6.54	down	0.00145
rc_T69020_s_at	T69020	3193	EST	5.39	down	0.00383
rc_T69029_f_at	T69029	3194	haptoglobin	33.18	down	0.02825
rc_T69164_at	T69164	3195	EST	4.38	down	0.00548
rc_T69284_s_at	T69284	3196	mannose-binding lectin (protein C) 2, soluble	36.53	down	0
rc_T69384_at	T69384	3198	period (Drosophila) homolog 1	5.88	down	0.01219
rc_T69728_at	T69728	3199	heat shock 90kD protein 1, beta	3.98	down	0.00786
rc_T70087_at	T70087	3200	EST	4.7	down	0.00173
rc_T71012_s_at	T71012	3201	fibrinogen, B beta polypeptide	43.61	down	0.00743
rc_T71021_at	T71021	3202	EST	6.74	down	0.0017
rc_T71373_at	T71373	3203	EST	83.08	down	0.00069
rc_T71776_at	T71776	3204	EST	10.3	down	0.00897
rc_T71978_at	T71978	3205	EST	4.39	down	0.0017

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_T72171_s_at	T72171	3206	thyroxin-binding globulin	10.41	down	0.00163
rc_T72268_s_at	T72268	3207	B-factor, proerdin	7.43	down	0.01197
rc_T72502_at	T72502	3208	EST	8.87	down	0.00009
rc_T72629_l_at	T72629	3209	EST	3.24	down	0.00556
rc_T72906_at	T72906	3210	EST	7.56	down	0.00062
rc_T73420_at	T73420	3211	short-chain dehydrogenase/reductase 1	4.58	down	0.00656
rc_T73433_s_at	T73433	3212	angiotensinogen	48.3	down	0.00049
rc_T73442_at	T73442	3213	EST	94.41	down	0
rc_T73739_s_at	T73739	3214	alanine-glyoxylate aminotransferase (oxalosis); hyperoxaluria 1; glycolicaciduria; serine-pyruvate	16.18	down	0.00277
rc_T74542_s_at	T74542	3215	UDP glycosyltransferase 2 family, polypeptide	32.36	down	0.00004
rc_T74608_at	T74608	3216	hydroxyacid oxidase (glycolate oxidase) 1	14.03	down	0
rc_T74884_f_at	T74884	3217	EST	3.76	down	0.02547
rc_T777729_f_at	T777729	3218	pyruvate carboxylase	7.29	down	0.00022
rc_T78433_s_at	T78433	3220	glycogen synthase 2 (liver)	8.62	down	0.00072
rc_T78889_s_at	T78889	3221	fibronectin 1	19.87	down	0.00912
rc_T79758_at	T79758	3224	EST	3.94	down	0.00581
rc_T79842_at	T79842	3225	EST	3.16	down	0.03159
rc_T79863_at	T79863	3226	EST	5.62	down	0.00074
rc_T81315_at	T81315	3227	EST	4.28	down	0.00187
rc_T82254_at	T82254	3229	EST	3.82	down	0.00091
rc_T82259_at	T82259	3230	EST	3.12	down	0.01122
rc_T82323_at	T82323	3231	immunoglobulin superfamily, member 4	10.14	down	0
rc_T83356_s_at	T83356	3232	apolipoprotein H (beta-2-glycoprotein I)	64.34	down	0.00802
T83397_at	T83397	3233	phytanoyl-CoA hydroxylase (Refsum disease)	63.6	down	0
T85532_f_at	T85532	3236	EST	4.33	down	0.00591
rc_T86664_at	T86664	3237	EST	3.17	down	0.00498
rc_T86482_at	T86482	3238	transferrin	11.15	down	0.00006
rc_T86978_s_at	T86978	3239	glutamate dehydrogenase 1	9.44	down	0.00006
rc_T87174_at	T87174	3240	EST	21.71	down	0.00681
rc_T90037_at	T90037	3246	EST	3.99	down	0.0016

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
rc_T90492_at	T90492	3248	EST	3.88	down	0.00454
rc_T90520_at	T90520	3249	EST	8.67	down	0.00072
rc_T90531_at	T90531	3250	EST	3.6	down	0.00301
rc_T90841_f_at	T90841	3251	EST	5.74	down	0.01876
rc_T91161_at	T91161	3253	EST	3.48	down	0.00002
rc_T91348_at	T91348	3254	EST	3.57	down	0.00011
rc_T92950_at	T92950	3256	EST	3.01	down	0.00497
rc_T94862_at	T94862	3258	EST	3.07	down	0.01417
rc_T95064_at	T95064	3260	EST	5.75	down	0.00604
rc_T95515_s_at	T95515	3261	KIAA0249 gene product	6.77	down	0.0001
rc_T95813_f_at	T95813	3262	KIAA1051 protein	38.38	down	0.00008
rc_T96969_at	T96969	3264	EST	3.42	down	0.00053
rc_T97234_at	T97234	3265	EST	4.34	down	0.00263
rc_T98199_l_at	T98199	3267	EST	4.86	down	0.00431
rc_T988676_at	T988676	3269	EST	46.94	down	0.0001
rc_T99636_s_at	T99636	3271	complement component 3 B-cell CLL/lymphoma 6 (zinc finger protein 51)	29.6	down	0.00051
U00115_at	U00115	3272	glucosidase-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease) solute carrier family 1 (glial high affinity glutamate	5.18	down	0.00045
U01120_at	U01120	3274	transporter), member 2 pre-B-cell colony-enhancing factor	13.41	down	0.00147
U01824_at	U01824	3276	cytochrome P450, subfamily IVF, polypeptide 2	3.2	down	0.00021
U02020_at	U02020	3277	hyaluronoglucosaminidase 1	3.37	down	0.01112
U02388_at	U02388	3278	proline-rich protein with nuclear targeting signal	9.38	down	0.00001
U03056_at	U03056	3280	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-	6.64	down	0
U03105_at	U03105	3281	hydroxysteroid dehydrogenase)	4.69	down	0.00017
U05861_at	U05861	3285	UDP glycosyltransferase 2 family, polypeptide	23.22	down	0.00002
U06641_s_at	U06641	3287	follistatin-like 1	24.32	down	0.00001
U06863_at	U06863	3288	complement component 8, alpha polypeptide	3.09	down	0.00091
U08006_s_at	U08006	3290	16	down	0.0011	

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
U08198_m1_at	U08198	3292	complement component 8, gamma polypeptide	19.71	down	0
U08854_s_at	U08854	3293	UDP glycosyltransferase 2 family, polypeptide	7.38	down	0.00005
U11313_at	U11313	3297	sterol carrier protein 2	5.44	down	0.00187
U12778_at	U12778	3301	acyl-Coenzyme A dehydrogenase, sulfotransferase family 2A,	5.68	down	0.00116
U13061_m1_at	U13061	3302	dehydroepiandrosterone (DHEA) -preferring, enoyl Coenzyme A hydratase 1, peroxisomal	11.32	down	0.00048
U16660_at	U16660	3313	stromal cell-derived factor 1	3.96	down	0.00002
U19495_s_at	U19495	3319	GTP cyclohydrolase 1 (dopa-responsive secreted phosphoprotein 2, 24kD)	4.59	down	0.00011
U19523_at	U19523	3320	dihydropyrimidine dehydrogenase	5.25	down	0.00029
U20530_at	U20530	3322	fructose-bisphosphatase 1	16.93	down	0
U20938_at	U20938	3324	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7	3.92	down	0.00053
U21931_at	U21931	3326	aldehyde dehydrogenase 4 (glutamate gamma-thio Redoxin peroxidase; pyrrole-5-nucleic acid, Interleukin 3 regulated UDP-glucose pyrophosphorylase 2)	3.4	down	0.00709
U22029_f_at	U22029	3327	solute carrier family 6 (neurotransmitter	71.98	down	0
U22961_s_at	U22961	3330	transporter, betaine/GABA), member 12	22.22	down	0.01531
U24266_at	U24266	3331	Down syndrome candidate region 1	14.54	down	0
U25182_at	U25182	3333	pigment epithelium-derived factor	3.13	down	0.02543
U26173_s_at	U26173	3335	transmembrane 4 superfamily member 4	6.4	down	0.00001
U27460_at	U27460	3339	apolipoprotein C-IV	11.46	down	0.00088
U27699_at	U27699	3340	tryptophan 2,3-dioxygenase	3.65	down	0.00381
U28833_at	U28833	3341	aldehyde dehydrogenase 9 (gamma-aminobutyrate dehydrogenase, E3	3.3	down	0.00306
U29953_m1_at	U29953	3342	EST	15.33	down	0.00212
U31449_at	U31449	3345	apolipoprotein C-IV	11.53	down	0.00187
U32576_m1_at	U32576	3347	tryptophan 2,3-dioxygenase	18.59	down	0.00005
U32576_m1_at	U32576	3347	aldehyde dehydrogenase 9 (gamma-	5.81	down	0.04343
U32989_at	U32989	3348	aminobutyrate dehydrogenase, E3	10.07	down	0.02825
U34252_at	U34252	3350	3.06	down	0.00613	
U36922_at	U36922	3352	down	0.01388		

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
U37055_ma1_s_at	U37055	macrophage stimulating 1 (hepatocyte growth factor-like), macrophage stimulating, pseudogene	18.28	down	0
U44111_at	U44111	histamine N-methyltransferase	3.5	down	0.00942
U46499_at	U46499	microsomal glutathione S-transferase 1	4.27	down	0.00244
U46689_at	U46689	aldehyde dehydrogenase 10 (fatty aldehyde protein tyrosine phosphatase type IVA, member 1)	3.5	down	0.01292
U48296_at	U48296	protein tyrosine phosphatase type IVA, member 1	4.25	down	0.02037
U48707_at	U48707	protein phosphatase 1, regulatory (inhibitor) 0	14.22	down	0
U48959_at	U48959	myosin, light polypeptide kinase	3.61	down	0.00084
U49082_at	U49082	transporter protein	9.17	down	0.00088
U49248_at	U49248	ATP-binding cassette, sub-family C (CFTR/MRP), 2,4-dienoyl CoA reductase 1, mitochondrial	7.06	down	0.00067
U49352_at	U49352	D-dopachrome tautomerase	5.41	down	0.02371
U49785_at	U49785	adenosine kinase	3.84	down	0.00044
U50196_at	U50196	EST	3.82	down	0.01425
U50527_s_at	U50527	betaine-homocysteine methyltransferase	3.93	down	0.00123
U50929_at	U50929	nicotinamide N-methyltransferase	36.91	down	0
U51010_s_at	U51010	hexokinase 3 (white cell)	27.79	down	0.00366
U51333_s_at	U51333	IQ motif containing GTPase activating protein 2	4.88	down	0.00055
U51903_at	U51903	ES1 (zebrafish) protein, human homolog of	3.23	down	0.00242
U53003_at	U53003	deoxyribonuclease I-like 3	4.84	down	0.00077
U56814_at	U56814	deoxyribonuclease I-like 3	29.43	down	0.00003
U56814_at	U56814	kynureninase (L-kynurenone hydrolase)	11.36	down	0.00001
U57721_at	U57721	sterol-C4-methyl oxidase-like	4.34	down	0.0197
U60205_at	U60205	isocitrate dehydrogenase 1 (NADP+)-soluble	5.16	down	0.00061
U62389_at	U62389	ATP-binding cassette, sub-family C (CFTR/MRP), lysophospholipase-like	3.15	down	0.03949
U66674_at	U66674	nuclear receptor subfamily 1, group H, member 4	6.13	down	0.00127
U67963_at	U67963	EST	3.19	down	0.00029
U68233_at	U68233	glutaryl-Coenzyme A dehydrogenase	6.76	down	0.00022
U68494_at	U68494	glutamic-pyruvate transaminase (alanine	4.82	down	0.00881
U69141_at	U69141	glutamic-pyruvate transaminase (alanine	3.06	down	0.00053
U70732_ma1_at	U70732	glutamic-pyruvate transaminase (alanine	27.63	down	0
U70732_ma1_at	U70732	5.64	down	0.00146	

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
U73514_at	U73514	3419	hydroxacyl-Coenzyme A dehydrogenase, type II	3.79	down	0.01392
U73682_at	U73682	3420	meningioma expressed antigen 6 (collod-coll)	3.08	down	0.01249
U76376_at	U76376	3425	harakiri, BCL2-interacting protein (contains only	11.77	down	0.00002
U77396_at	U77396	3426	LPS-induced TNF-alpha factor	4.47	down	0.00108
U77594_at	U77594	3428	retinoic acid receptor responder (tazarotene	11.95	down	0.00527
U78190_mna1_at	U78190	3431	GTP cyclohydrolase I feedback regulatory protein	3.94	down	0.034
U79294_at	U79294	3435	Phosphatidic acid phosphatase type 2b	3.13	down	0.00129
U79303_at	U79303	3436	protein predicted by clone 23882	4.45	down	0
U79716_at	U79716	3437	reelin	3.51	down	0.00053
U82108_s_at	U82108	3441	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 2	3.19	down	0.01545
U82468_at	U82468	3442	tubby like protein 1	3.34	down	0.0097
U84569_at	U84569	3445	chromosome 21 open reading frame 2	3.46	down	0.01844
U86529_at	U86529	3451	glutathione S-transferase zeta 1	3.41	down	0.0118
U90544_at	U90544	3454	solute carrier family 17 (sodium phosphate),	6.42	down	0.00023
U90545_at	U90545	3455	solute carrier family 17 (sodium phosphate),	4.14	down	0.00005
U95090_at	U95090	3464	nephrosis 1, congenital, Finnish type (nephrin)	14.01	down	0.00018
U95090_at	U95090	3464	nephrosis 1, congenital, Finnish type (nephrin)	7.44	down	0.00004
W03796_at	W03796	3468	EST	8.3	down	0.0032
W07723_at	W07723	3471	EST	3.51	down	0.00026
W15528_at	W15528	3475	EST	3.56	down	0.00424
W20094_at	W20094	3477	DKFZP586A0522 protein	38.09	down	0.00188
W20276_f_at	W20276	3478	EST	3.82	down	0.00033
rc_W20467_f_at	W20467	3480	EST	7.76	down	0.00008
rc_W15528_at	W26769	3483	CG1-86 protein	8.14	down	0.00204
rc_W20094_at	W26996	3484	EST	6.42	down	0.00005
rc_W20467_f_at	W27023	3485	neuroendocrine-specific protein C like (foocen)	6.79	down	0.00805
rc_W20467_f_at	W28798	3492	phosphodiesterase 6A, cGMP-specific, rod, alpha	7.01	down	0.00017
rc_W20467_f_at	W28824	3493	EST	15.8	down	0.00006
rc_W20467_f_at	W28944	3494	EST	37.07	down	0.00205
rc_W31478_s_at	W31478	3496	EST	3.36	down	0.01511

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_W33167_at	W33167	3499 EST	8.01	down	0.00026
W35309_at	W35309	3500 EST	3.11	down	0.029
W36290_s_at	W36290	3501 Kreisler (mouse) maf-related leucine zipper	3.94	down	0.02718
rc_W37382_at	W37382	3502 EST	4.37	down	0.00677
rc_W38407_at	W38407	3506 EST	4.17	down	0.00392
rc_W42483_at	W42483	3510 EST	3.04	down	0.02518
rc_W42789_at	W42789	3515 EST	9.38	down	0.00059
rc_W42996_at	W42996	3517 EST	6.18	down	0.00587
rc_W44745_at	W44745	3520 EST	9.02	down	0.00276
rc_W45051_at	W45051	3521 EST	4.68	down	0.00433
W45259_at	W45259	3522 EST	3.78	down	0.00069
rc_W45560_at	W45560	3525 EST	5.06	down	0.00996
rc_W46391_at	W46391	3527 alpha integrin binding protein 63	4.03	down	0.01363
rc_W46404_at	W46404	3528 EST	3.73	down	0.00116
rc_W47175_at	W47175	3534 3-prime-phosphoadenosine 5-prime-deaminase	5.54	down	0.00914
rc_W51951_s_at	W51951	3542 CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal leucine aminopeptidase)	3.14	down	0.01691
W52581_at	W52581	3543 adipose differentiation-related protein; adipophilin	3.08	down	0.00091
W52821_at	W52821	3544 leucine aminopeptidase	4.02	down	0.03787
W55903_at	W55903	3546 adipose differentiation-related protein; adipophilin	9.12	down	0.00459
rc_W57821_at	W57821	3548 EST	5.03	down	0.00277
W58540_at	W58540	3553 KIAA1131 protein	4.28	down	0.0184
rc_W58756_at	W58756	3554 EST	12.17	down	0.00087
rc_W60002_s_at	W60002	3555 plastin 3 (T isoform)	4.88	down	0.01694
rc_W60186_at	W60186	3557 EST	3.24	down	0.00228
rc_W61000_at	W61000	3560 EST	3.15	down	0.03143
rc_W61319_at	W61319	3561 EST	3.02	down	0.00031
W61377_at	W61377	3562 EST	9.33	down	0.0012
rc_W61378_s_at	W61378	3563 EST	8.31	down	0
rc_W63728_at	W63728	3565 EST	5.03	down	0.00311
rc_W63785_at	W63785	3567 EST	3.91	down	0.04089

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_W67147_at	W67147	35668	deleted in liver cancer 1	9.74	down	0.00002
rc_W67199_at	W67199	35669	EST	3.09	down	0.01528
rc_W67564_s_at	W67564	3571	nuclear receptor subfamily 0, group B, member 2	30.34	down	0
rc_W68721_f_at	W68721	3572	cleft lip and palate associated transmembrane	6.34	down	0.01504
rc_W69675_at	W69675	3575	EST	4.42	down	0.00019
rc_W70115_s_at	W70115	3576	histidine ammonia-lyase	11.65	down	0.0003
rc_W70313_at	W70313	3578	EST	3	down	0.00643
rc_W72044_at	W72044	3580	insulin induced gene 1	24.58	down	0.00001
rc_W72079_at	W72079	3581	EST	6.36	down	0.00641
rc_W72972_at	W72972	3587	EST	5.61	down	0.00939
rc_W73194_at	W73194	3590	dermatopontin	3.45	down	0.02211
rc_W73601_at	W73601	3592	EST	32.25	down	0
rc_W73818_at	W73818	3593	EST	4.32	down	0.00385
rc_W73889_s_at	W73889	3594	ttranectin (plasminogen-binding protein)	7.45	down	0.00091
W74158_at	W74158	3596	EST	4.81	down	0.00233
W78046_at	W79046	3602	peroxisomal D3,D2-enoyl-CoA Isomerase	27.9	down	0.00023
rc_W79422_s_at	W79422	3604	fumarylacetoacetate	14.94	down	0.00059
rc_W80609_at	W80609	3606	EST	4.68	down	0.01729
W81053_at	W81053	3610	EST	4.91	down	0.00164
rc_W81079_at	W81079	3611	EST	3.31	down	0.0167
W81268_at	W81268	3612	protein kinase, interferon-inducible double stranded RNA dependent	4.2	down	0.00007
rc_W85765_at	W85765	3618	EST	3.83	down	0.00379
rc_W85847_at	W85847	3619	EST	7.28	down	0.00024
rc_W85886_at	W85886	3621	EST	3.46	down	0.00814
rc_W85888_at	W85888	3622	EST	3.99	down	0.00697
rc_W86075_at	W86075	3624	EST	13.83	down	0.00057
rc_W86375_s_at	W86375	3626	EST	19.29	down	0.0061
rc_W86431_s_at	W86431	3627	protein C Inhibitor (plasminogen activator inhibitor	14.94	down	0.00152
rc_W86600_at	W86600	3628	EST	32.14	down	0
rc_W86756_at	W86756	3630	retinoid X receptor, alpha	3.77	down	0.02472

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_W86850_f_at	W86850	3631	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	4.9	down	0.03105
rc_W87454_at	W87454	3632	homogenitase 1,2-dioxygenase (homogenitase)	7.93	down	0.00149
rc_W87480_at	W87480	3633	STAT Induced STAT Inhibitor-2	3.24	down	0.01063
rc_W87532_at	W87532	3634	putative glycine-N-acyltransferase	12.34	down	0.00014
rc_W87606_s_at	W87606	3635	protein Z, vitamin K-dependent plasma	9.23	down	0.00085
rc_W87781_at	W87781	3636	EST	6.1	down	0.00045
rc_W87824_at	W87824	3637	EST	3.67	down	0.01559
rc_W88568_at	W88568	3638	glycogenin 2	4.16	down	0.00111
rc_W88946_at	W88946	3639	putative glycine-N-acyltransferase	58.26	down	0
rc_W88985_at	W88985	3640	KIAA0903 protein	3.94	down	0.00295
rc_W89178_at	W89178	3641	transferrin receptor 2	10.85	down	0.00116
rc_W90128_s_at	W90128	3643	X-box binding protein 1	10.04	down	0.00018
rc_W90455_s_at	W90455	3646	alpha-2-macroglobulin	10.35	down	0.00063
rc_W90560_at	W90560	3647	EST	3.35	down	0.00388
rc_W90583_r_at	W90583	3648	EST	4.35	down	0.00318
rc_W90766_at	W90766	3649	EST	7.58	down	0.00057
rc_W92148_s_at	W92148	3650	kliningen	51.09	down	0.00376
rc_W92213_at	W92213	3654	EST	16.55	down	0.00097
rc_W92271_s_at	W92271	3655	glycine cleavage system protein H (aminomethyl	4.36	down	0.0064
rc_W94427_at	W94427	3659	EST	3.86	down	0.02649
rc_W94942_i_at	W94942	3661	dual specificity phosphatase 10	7.23	down	0.00137
rc_W95041_at	W95041	3662	EST	12.79	down	0.00001
W95795_at	W95795	3665	EST	7.8	down	0.00359
X00129_at	X00129	3667	retinol-binding protein 4, [Interstitial	18.57	down	0.02378
AFFX-HSAC07/X00351_M_st	X00351	3668	actin, beta	4.76	down	0.0003
X01038_ma1_s_at	X01038	3669	apolipoprotein A-I, apolipoprotein C-III	19.97	down	0.0275
X01388_at	X01388	3670	apolipoprotein C-III	10.9	down	0.01246
X02160_at	X02160	3671	insulin receptor	5.29	down	0.0001
X02160_at	X02160	3671	insulin receptor	3.27	down	0.0007
X02176_s_at	X02176	3672	complement component 9	9.61	down	0.0004

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
X02750_at	X02750	3673	protein C (inactivator of coagulation factors Va vitronectin (serum spreading factor, somatomedin B, complement S-protein)	7.04	down	0.00079
X03168_at	X03168	3674	alcohol dehydrogenase 2 (class I), beta	25.88	down	0.00911
X03350_at	X03350	3676	catalase	19.32	down	0.00001
X04085_ma1_at	X04085	3678	gap junction protein, beta 1, 32kD (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked)	11.27	down	0.0002
X04325_at	X04325	3679	plasminogen activator inhibitor, type I	10.17	down	0.00061
X04729_s_at	X04729	3682	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	3.15	down	0.01337
X04828_at	X04828	3683	aldehyde dehydrogenase 2, mitochondrial	5.22	down	0.01278
X05409_at	X05409	3684	growth hormone receptor	3.99	down	0.01029
X06562_at	X06562	3686	inter-alpha (globulin) inhibitor, H2 polypeptide	10.87	down	0.00001
X07173_at	X07173	3690	cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolising), polypeptide 7a	30.3	down	0.00016
X07618_s_at	X07618	3691	cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolising), polypeptide 7a	35.79	down	0.00065
X07618_s_at	X07618	3691	cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolising), polypeptide 7a	13.58	down	0
X07619_s_at	X07619	3692	hepsin (transmembrane protease, serine 1)	4.96	down	0.00004
X07732_at	X07732	3693	protein kinase, cAMP-dependent, catalytic, alpha	28.21	down	0
X07767_at	X07767	3694	arginase, liver	5.94	down	0.00028
X12662_ma1_at	X12662	3697	D-amino-acid oxidase	20.59	down	0
X13227_at	X13227	3698	CD14 antigen	4.81	down	0.0002
X13334_at	X13334	3699	cytochrome P450, subfamily IIA (phenobarbital- inducible), polypeptide 6	12.77	down	0.000887
X13930_f_at	X13930	3700	pre-alpha (globulin) inhibitor, H3 polypeptide	38.52	down	0
X14690_s_at	X14690	3703	thrombospondin 1	16.07	down	0.00438
X14787_at	X14787	3704	acetyl-Coenzyme A acyltransferase 1	3.69	down	0.01115
X14813_at	X14813	3705	(peroxisomal 3-oxoacyl-Coenzyme A thiolase)	11.61	down	0.0002
X15422_at	X15422	3708	mannose-binding lectin (protein C) 2, soluble	8.29	down	0.00015

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	P value
X16260_s_at	X16260	Inter-alpha (globulin) inhibitor, H1 polypeptide	44.65	down	0.000933
X16260_s_at	X16260	Inter-alpha (globulin) inhibitor, H1 polypeptide	26.39	down	0.0004
X16349_s_at	X16349	sex hormone-binding globulin	9.34	down	0.00007
X17025_at	X17025	isopentenyl-diphosphate delta isomerase	3.13	down	0.00043
		paired basic amino acid cleaving enzyme (furin)			
X17094_at	X17094	membrane associated receptor protein)	8.5	down	0
X52150_ma1_s_at	X52150	arylsulfatase A	3.51	down	0.00113
X52520_at	X52520	tyrosine aminotransferase	13.51	down	0.00002
X52541_at	X52541	early growth response 1	3.77	down	0.00894
		alanine-glyoxylate aminotransferase (oxalosis I);			
X53414_at	X53414	hyperoxaluria I; glycollacaciduria; serine-pyruvate	13.87	down	0.00003
X53595_s_at	X53595	apolipoprotein H (beta-2-glycoprotein I)	27.28	down	0.0066
X54380_at	X54380	pregnancy-zone protein	8.44	down	0.00059
		asialoglycoprotein receptor 2			
X55283_ma1_s_at	X55283	alcohol dehydrogenase 4 (class II), pi polypeptide	84.99	down	0.00084
X56411_ma1_at	X56411	pregnancy-zone protein	25.14	down	0.00144
X56692_at	X56692	C-reactive protein, pentraxin-related	15.15	down	0.01884
X57025_at	X57025	insulin-like growth factor 1 (somatomedin C)	4.72	down	0.00087
X58022_at	X58022	corticotropin releasing hormone-binding protein	4.09	down	0.000076
X58528_s_at	X58528	ATP-binding cassette, sub-family D (ALD),	4.91	down	0.00728
X59766_at	X59766	alpha-2-glycoprotein 1, zinc	12.96	down	0.00043
		cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis),			
X59812_at	X59812	glutamate-ammonia ligase (glutamine synthase)	4.65	down	0.036
X59834_at	X59834	adenylate kinase 3	4.29	down	0.00255
X60673_s_at	X60673	B-cell translocation gene 1, anti-proliferative	8.3	down	0.00016
X61123_at	X61123	sialyltransferase 1 (beta-galactoside alpha-2,6-	3.2	down	0.00796
X62822_at	X62822	UDP glycosyltransferase 2 family, polypeptide	4.89	down	0.00274
X63359_at	X63359	H factor (complement)-like 3	13.66	down	0.00051
X64877_at	X64877	H factor (complement)-like 3	14.6	down	0
X64877_s_at	X64877	Glutathione S-transferase A2, glutathione S-	12.33	down	0
X65727_cds2_s_at	X65727	cytochrome P450, subfamily IIC (mephenytoin 4-	73.64	down	0
X65962_s_at	X65962		5.47	down	0.00014

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
X67235_s_at	X67235	3773	hematopoietically expressed homeobox	3.17	down	0.0045
X67491_f_at	X67491	3776	glutamate dehydrogenase 1	7.45	down	0.00019
X68277_at	X68277	3777	dual specificity phosphatase 1	6.68	down	0.0036
X68679_s_at	X68679	3779	complement factor H related 3, complement factor	38.22	down	0.00036
X68733_m1_at	X68733	3781	alpha-1-antichymotrypsin	7.87	down	0.03266
X72012_at	X72012	3789	endoglin (Osler-Rendu-Weber syndrome 1)	4.2	down	0.005
X72177_m1_at	X72177	3790	complement component 6	12.94	down	0.00011
X75252_at	X75252	3793	prostatic binding protein	3.78	down	0.00231
X76105_at	X76105	3794	death-associated protein	3.02	down	0.00944
X76648_at	X76648	3796	glutaredoxin (thioltransferase)	4	down	0.00211
X76717_at	X76717	3797	metallothionein 1L	8.09	down	0.00025
X77548_at	X77548	3798	nuclear receptor coactivator 4	3.76	down	0.00758
X78706_at	X78706	3801	carrilin acetyltransferase	4.85	down	0.00442
X78992_at	X78992	3802	butyrate response factor 2 (EGF-response factor	4.69	down	0.01995
X83416_s_at	X83416	3811	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Sträussler-Scheinker syndrome, fatal 3-hydroxy-3-methylglutaryl-Coenzyme A synthase	3.28	down	0.00221
X83618_at	X83618	3813	2 (mitochondrial)	6.27	down	0.02099
X85116_m1_s_at	X85116	3814	erythrocyte membrane protein band 7.2	6.37	down	0.00356
X86401_s_at	X86401	3815	glycine amidinotransferase (L-arginine:glycine	22.7	down	0
X87344_cds10_r_at	X87344	3817	EST	3.04	down	0.02779
X90579_s_at	X90579	3819	EST	29.82	down	0.00273
X90999_at	X90999	3820	hydroxyacyl glutathione hydrolase; glyoxalase 2	5.27	down	0.00047
X91148_at	X91148	3821	microsomal triglyceride transfer protein (large	5.91	down	0.00045
X92720_at	X92720	3826	phosphoenolpyruvate carboxykinase 2	7.6	down	0.00001
X92744_at	X92744	3827	defensin, beta 1	4.96	down	0.01804
X94563_xp12_r_at	X94563	3831	EST	3.52	down	0.00928
X95190_at	X95190	3832	acyl-Coenzyme A oxidase 2, branched chain	12.81	down	0
X95384_at	X95384	3833	translational inhibitor protein p14.5	17.69	down	0.00048
X95715_at	X95715	3835	ATP-binding cassette, sub-family C (CFTR/MRP),	6.78	down	0.00045
X95876_at	X95876	3836	G protein-coupled receptor 9	3.12	down	0.001

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
X96752_at	X96752	3837	L-3-hydroxyacyl-Coenzyme A dehydrogenase; adipophilin	4.94	down	0.00359
X97324_at	X97324	3839	adipose differentiation-related protein; adipophilin	5.97	down	0.04638
X98337_s_at	X98337	3840	complement factor H related 3,complement factor	13.5	down	0.00001
Y00097_s_at	Y00097	3844	annexin A6	3.4	down	0.00233
Y00317_at	Y00317	3845	UDP glycosyltransferase 2 family, polypeptide B4	18.34	down	0.00001
Y00317_at	Y00317	3845	UDP glycosyltransferase 2 family, polypeptide B4	8.97	down	0.00025
Y00318_at	Y00318	3846	I factor (complement)	10	down	0.00019
Y00339_s_at	Y00339	3847	carbonic anhydrase II	6.89	down	0
Y00451_s_at	Y00451	3848	aminolevulinic, delta-, synthase 1	10.52	down	0.00107
Y08374_m1_at	Y08374	3853	chitinase 3-like 1 (cartilage glycoprotein-39)	3.5	down	0.04208
Y08409_at	Y08409	3854	thyroid hormone responsive SPOT14 (rat)	5.84	down	0.00455
Y09616_at	Y09616	3857	carboxylesterase 2 (intestine, liver)	18.78	down	0.00026
Y10032_at	Y10032	3858	serum/glucocorticoid regulated kinase	4.24	down	0.00148
Y10659_at	Y10659	3859	Interleukin 13 receptor, alpha 1	4.22	down	0.00061
Y10659_at	Y10659	3859	interleukin 13 receptor, alpha 1	3.17	down	0.00095
Y12711_at	Y12711	3861	progesterone binding protein	14.83	down	0.00285
Z11559_at	Z11559	3862	iron-responsive element binding protein 1	4.3	down	0.00066
Z11737_at	Z11737	3863	flavin containing monooxygenase 4	3.84	down	0.00043
Z11737_at	Z11737	3863	flavin containing monooxygenase 4	3.67	down	0.00632
Z11793_at	Z11793	3864	selenoprotein P, plasma, 1 branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disease)	9.94	down	0.00021
Z14093_at	Z14093	3865		3.24	down	0.00301
Z20777_at	Z20777	3866	EST	29.59	down	0.00044
Z24459_m1_at	Z24459	3869	mature T-cell proliferation 1	5.29	down	0.00001
Z24725_at	Z24725	3870	mitogen inducible 2	7.9	down	0
Z26491_s_at	Z26491	3873	catechol-O-methyltransferase	3.08	down	0.00877
Z28339_at	Z28339	3875	aldo-keto reductase family 1, member D1 (delta 4-	24.66	down	0
Z29481_at	Z29481	3877	3-hydroxyanthranilate 3,4-dioxygenase	6.39	down	0.00029
Z29481_at	Z29481	3877	3-hydroxyanthranilate 3,4-dioxygenase	3.64	down	0.000096
Z30425_at	Z30425	3878	nuclear receptor subfamily 1, group I, member 3	26.64	down	0

Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
Z30425_at	Z30425	3878 nuclear receptor subfamily 1, group I, member 3	7.88	down	0.00006
Z31357_at	Z31357	3880 cysteine dioxygenase, type I	11.2	down	0.0001
Z31690_s_at	Z31690	3881 lipase A, lysosomal acid, cholesterol esterase	3.83	down	0.00103
rc_Z38161_at	Z38161	3884 EST	4.38	down	0.0011
rc_Z38192_s_at	Z38192	3885 EST	3.35	down	0.00184
rc_Z38435_at	Z38435	3890 ribosomal protein L21	3.12	down	0.03617
rc_Z38777_f_at	Z38777	3895 nuclear receptor binding factor-2	3.28	down	0.022
rc_Z39059_at	Z39059	3899 EST	5.19	down	0.0014
rc_Z39406_at	Z39406	3905 nuclear receptor co-repressor 1	4.18	down	0.00439
rc_Z39431_at	Z39431	3907 KIAA1086 protein	3.68	down	0.0013
rc_Z39476_at	Z39476	3908 EST	5.9	down	0.00687
rc_Z39622_s_at	Z39622	3910 EST	4.4	down	0.00001
rc_Z39818_at	Z39818	3912 EST	3.26	down	0.00089
rc_Z39833_at	Z39833	3913 GTP-binding protein	16.89	down	0.00034
rc_Z39976_at	Z39976	3915 EST	5.76	down	0.00012
rc_Z39978_at	Z39978	3916 EST	3.56	down	0.04051
rc_Z40192_at	Z40192	3918 EST	3.89	down	0.00223
rc_Z40259_s_at	Z40259	3919 EST	8.18	down	0.00002
rc_Z40305_at	Z40305	3920 EST	6.45	down	0.00001
rc_Z40715_at	Z40715	3923 delta-6 fatty acid desaturase	18.68	down	0.0007
rc_Z40902_at	Z40902	3926 SEC14 (S. cerevisiae)-like 2	12.87	down	0.00001
rc_Z41042_at	Z41042	3928 EST	3.63	down	0.00943
Z47553_at	Z47553	3939 flavin containing monooxygenase 5	6.17	down	0.00011
Z48199_at	Z48199	3942 syndecan 1	4.43	down	0.00408
Z48475_at	Z48475	3943 glucokinase (hexokinase 4) regulatory protein	13.84	down	0
Z49269_at	Z49269	3945 small inducible cytokine subfamily A (Cys-Cys),	18.46	down	0.00001
Z49878_at	Z49878	3946 guanidinoacetate N-methyltransferase	13.96	down	0.00021
Z69923_at	Z69923	3948 HGF activator	11.37	down	0.00053
Z80345_mna1_s_at	Z80345	3951 acyl-Coenzyme A dehydrogenase, C-2 to C-3	5.93	down	0.0024
Z84718_cds1_at	Z84718	3952 EST	3.26	down	0.02252
Z84721_cds2_at	Z84721	3953 hemoglobin, zeta	8.77	down	0.01446

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	P value
rc_AA005358_at	AA005358	14 EST	5.51	down	0.00059
rc_AA007395_s_at	AA007395	17 alcohol dehydrogenase 4 (class II), pi polypeptide	37.78	down	0.00939
rc_AA007629_at	AA007629	19 EST	5.56	down	0.00005
rc_AA010205_at	AA010205	23 EST	5.71	down	0.00014
rc_AA010605_s_at	AA010605	26 4-hydroxyphenylpyruvate dioxygenase	25.52	down	0.00855
rc_AA010619_at	AA010619	27 EST	5.28	down	0.002
rc_AA018822_s_at	AA018822	40 core promoter element binding protein	3.39	down	0.01801
rc_AA035245_s_at	AA035245	79 aldehyde oxidase 1	7.97	down	0.02387
rc_AA035457_at	AA035457	80 EST	3.41	down	0.00968
rc_AA039335_s_at	AA039335	89 coagulation factor XII (Hageman factor)	5.33	down	0.03807
rc_AA039616_at	AA039616	90 EST	3.84	down	0.00997
rc_AA046457_at	AA046457	111 EST	3.05	down	0.02078
rc_AA046747_at	AA046747	114 EST	4.77	down	0.00023
rc_AA056482_at	AA056482	141 EST	3.06	down	0.01313
rc_AA057678_at	AA057678	143 EST	6.63	down	0.00089
rc_AA069696_at	AA069696	150 EST	3.07	down	0.01569
rc_AA070191_at	AA070191	154 EST	3.24	down	0.00216
rc_AA074885_at	AA074885	161 macrophage receptor with collagenous structure	10.88	down	0.00087
rc_AA076326_at	AA076326	170 SEC14 (S. cerevisiae)-like 2	3.85	down	0.0349
rc_AA076383_at	AA076383	171 EST	4.65	down	0.00593
rc_aa084668_at	AA084668	180 ubiquitin-like 3	4.74	down	0.02055
rc_AA085987_s_at	AA085987	183 UDP glycosyltransferase 1	3.03	down	0.03035
AA090257_at	AA090257	190 superoxide dismutase 2, mitochondrial	5.11	down	0.02774
AA090439_at	AA090439	192 ribosomal protein S6	6.59	down	0.01108
rc_AA099225_at	AA099225	206 EST	4.18	down	0.00064
rc_AA100026_at	AA100026	211 EST	4.36	down	0.00567
rc_AA112101_f_at	AA112101	222 EST	3.75	down	0.03175
rc_AA122345_f_at	AA122345	238 glutamate dehydrogenase 1	4.03	down	0.01058
rc_AA129390_at	AA129390	262 EST	3.45	down	0.00128
rc_AA142849_at	AA142849	306 EST	3.19	down	0.03495
rc_aa147646_s_at	AA147646	317 DKFZP586A0522 protein	3.19	down	0.00508

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA150776_at	AA150776	330	EST	6.17	down	0.00004
rc_AA151676_at	AA151676	337	peptidyl arginine deiminase, type II aldo-keto reductase family 7, member A2 (afatoxin aldehyde reductase)	3.85	down	0.00875
rc_AA157799_at	AA157799	348	estrogen receptor 1	3.08	down	0.00207
rc_AA164586_s_at	AA164586	359	aldehyde reductase	3.56	down	0.01231
rc_AA167565_at	AA167565	362	EST	3.81	down	0.04057
rc_AA172372_at	AA172372	370	EST	5.12	down	0.00032
rc_AA182030_at	AA182030	387	EST	3.51	down	0.0403
AA188921_at	AA188921	393	similar to <i>Caenorhabditis elegans</i> protein C42C1.9	3.38	down	0.00862
rc_AA194997_s_at	AA194997	412	EST	4.8	down	0.00153
rc_AA196287_at	AA196287	420	EST	4.86	down	0.01656
rc_AA210850_at	AA210850	431	EST	3.12	down	0.00288
rc_AA223902_at	AA223902	450	EST	4.22	down	0.01315
rc_AA232114_s_at	AA232114	463	epoxide hydrolase 2, cytoplasmic	6.18	down	0.00231
rc_AA233152_at	AA233152	467	EST	5.8	down	0.00272
rc_AA233837_at	AA233837	474	EST	3.46	down	0.01365
rc_AA235310_at	AA235310	496	EST	7.08	down	0.04056
rc_AA236401_at	AA236401	510	EST	5.31	down	0.01787
rc_AA236455_r_at	AA236455	512	EST	6.73	down	0.02418
rc_AA236455_s_at	AA236455	512	EST	5.1	down	0.00307
rc_AA253216_at	AA253216	561	EST	4.14	down	0.0014
rc_AA253369_s_at	AA253369	563	EST	5.64	down	0.00478
rc_AA256367_s_at	AA256367	579	paraoxonase 3	8.37	down	0.02326
rc_AA258350_at	AA258350	592	EST	4.1	down	0.02962
rc_AA279676_s_at	AA279676	630	deoxyribonuclease I-like 3	10.52	down	0.00181
rc_AA282061_at	AA282061	652	KIAA0962 protein	3.46	down	0.00698
rc_AA282886_at	AA282886	663	EST	3.29	down	0.00025
rc_AA284795_at	AA284795	678	phosphatidylethanolamine N-methyltransferase	5.7	down	0.00004
rc_AA285053_at	AA285053	681	EST	5	down	0.00718
rc_AA287122_at	AA287122	686	EST	5.21	down	0.00523
rc_AA287566_at	AA287566	690	KIAA0187 gene product	6.99	down	0.00023

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Sq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA291749_s_at	AA291749	703	estrogen receptor 1	5.06	down	0.00044
rc_AA297532_f_at	AA297532	725	EST	5.01	down	0.00745
rc_AA343142_at	AA343142	751	EST	5.79	down	0.02747
rc_AA348922_s_at	AA348922	758	fatty-acid-Coenzyme A ligase, long-chain 1,fatty-acid-	11.4	down	0.00848
AA376875_at	AA376875	770	Coenzyme A ligase, long-chain 2	3.45	down	0.00105
rc_AA377087_at	AA377087	771	monoamine oxidase A	4.61	down	0.01616
AA397841_at	AA397841	780	EST	3.29	down	0.00825
rc_AA398892_at	AA398892	800	similar to yeast BET3 (<i>S. cerevisiae</i>)	4.33	down	0.01326
AA400177_at	AA400177	808	EST	3.21	down	0.03901
rc_AA401376_at	AA401376	829	EST	3.39	down	0.01403
rc_AA401562_s_at	AA401562	830	EST	7.97	down	0.00527
rc_AA402224_at	AA402224	836	growth arrest and DNA-damage-inducible, gamma	3.66	down	0.0033
rc_AA404487_at	AA404487	851	EST	3.01	down	0.0059
rc_AA417046_at	AA417046	915	fatty-acid-Coenzyme A ligase, very long-chain 1	8.49	down	0.02476
			small inducible cytokine subfamily B (Cys-X-Cys),			
rc_AA426640_at	AA426640	969	member 14 (BRAK)	4.8	down	0.00539
rc_AA428325_at	AA428325	988	EST	4.09	down	0.02486
rc_AA433946_at	AA433946	1033	EST	10.24	down	0.00663
rc_AA435746_f_at	AA435746	1043	GTPase activating protein-like	4.21	down	0.03192
rc_AA435985_at	AA435985	1049	EST	3.86	down	0.01713
AA42334_at	AA42334	1069	EST	3.02	down	0.01936
rc_AA446864_at	AA446864	1095	EST	11.57	down	0.00001
rc_AA448002_at	AA448002	1113	putative type II membrane protein	14.14	down	0
			FXYD domain-containing ion transport regulator 1			
rc_AA448300_at	AA448300	1116	(phospholemman)	9.27	down	0.00108
rc_AA450114_at	AA450114	1131	EST	3.29	down	0.01171
rc_AA450127_at	AA450127	1132	growth arrest and DNA-damage-inducible, beta	3.37	down	0.00647
rc_AA453988_at	AA453988	1160	methionine adenosyltransferase I, alpha	7.78	down	0.02695
rc_AA454733_s_at	AA454733	1169	EST	5.73	down	0.00748
rc_AA455367_at	AA455367	1176	DKFZP586F1018 protein	3.47	down	0.00138

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA455988_at	AA455988	1184	butyrobetaine (gamma), 2-oxoglutarate dioxygenase	12.51	down	0
rc_AA458652_at	AA458652	1202	(gamma-butyrobetaine hydroxylase)	5.03	down	0.00065
rc_AA460012_at	AA460012	1224	solute carrier family 22 (extraneuronal monoamine transporter), member 3	3.73	down	0.0313
rc_AA460449_at	AA460449	1228	EST	3.53	down	0.01247
rc_AA460661_at	AA460661	1229	EST	5.46	down	0.00151
rc_AA461444_at	AA461444	1239	EST	3.19	down	0.02844
rc_AA465233_s_at	AA465233	1269	succinate-CoA ligase, GDP-forming, beta subunit	3.19	down	0.00036
rc_AA477119_at	AA477119	1289	EST	4.62	down	0.00072
AA477919_at	AA477919	1293	EST	3.9	down	0.00265
rc_AA478298_s_at	AA478298	1297	adipose specific 2	5.29	down	0.00943
rc_AA480991_s_at	AA480991	1323	EST	4.83	down	0.03498
AA486511_at	AA486511	1349	EST	3.9	down	0.01409
rc_AA490620_at	AA490620	1378	EST	6.25	down	0.03613
rc_AA599472_at	AA599472	1451	succinate-CoA ligase, GDP-forming, beta subunit	3.31	down	0.02619
rc_AA599814_at	AA599814	1456	EST	4.09	down	0.00235
rc_AA599937_s_at	AA599937	1458	insulin-like growth factor-binding protein 4	6.31	down	0.0477
rc_AA608802_at	AA608802	1470	EST	3.44	down	0.01709
rc_AA608837	AA608837	1472	EST	5.15	down	0.00005
rc_AA609519_at	AA609519	1482	EST	5.23	down	0.00068
rc_AA609537_s_at	AA609537	1483	hepatocellular carcinoma factor	4.88	down	0.00118
rc_AA621131_at	AA621131	1513	EST	4.57	down	0.03867
rc_AA621209_at	AA621209	1516	similar to <i>Caenorhabditis elegans</i> protein C42C1.9	4.01	down	0.00563
C02386_s_at	C02386	1561	hypothetical protein	3.66	down	0.00673
C02460_at	C02460	1562	EST	3.92	down	0.03073
rc_C20653_at	C20653	1578	EST	4.32	down	0.00718
rc_C20810_at	C20810	1579	EST	3.57	down	0.02116
rc_C21130_at	C21130	1583	cytochrome P450, subfamily IIIA (naphedipine oxidase), polypeptide 3	3.24	down	0.03355
D00003_at	D00003	1586		9.46	down	0.00001

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
D00003_s_at	D00003	1586	cytochrome P450, subfamily IIIA (naphthalene oxidase), polypeptide 3	6.8	down	0.01328
D00408_s_at	D00408	1589	cytochrome P450, subfamily IIIA (naphthalene oxidase), polypeptide 3, cytochrome P450, subfamily IIIA (naphthalene oxidase), polypeptide 3, cytochrome P450, subfamily IIIA (naphthalene oxidase), polypeptide 5, cytochrome P450, subfamily IIIA, polypeptide 7	3.58	down	0.02048
D10040_at	D10040	1593	fatty-acid-Coenzyme A ligase, long-chain 2	4.15	down	0.02947
rc_D11756_f_at	D11756	1596	EST	4.08	down	0.02972
D12620_s_at	D12620	1601	cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase)	6.03	down	0.03947
D12620_s_at	D12620	1601	cytochrome P450, subfamily IVF, polypeptide 2, cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase)	4.7	down	0.04091
D13243_s_at	D13243	1602	pyruvate kinase, liver and RBC	5.58	down	0.04029
D13705_s_at	D13705	1610	cytochrome P450, subfamily IVA, polypeptide 11	3.3	down	0.0051
D14012_s_at	D14012	1612	HGF activator	7.27	down	0.00145
D31628_s_at	D31628	1646	4-hydroxyphenylpyruvate dioxygenase	13.18	down	0.02064
rc_D45529_at	D45529	1662	EST	3.01	down	0.03105
D49357_at	D49357	1665	methionine adenosyltransferase I, alpha	4.85	down	0.04435
rc_D62518_at	D62518	1708	EST	5.96	down	0.00027
D63160_at	D63160	1709	ficolin (collagen/fibrinogen domain-containing lectin) 2 (hucolin)	3.72	down	0.00312
D78011_at	D78011	1717	dihydropyrimidinase	5.54	down	0.0312
D78725_at	D78725	1720	KIAA0914 gene product	3.19	down	0.01083
D79276_at	D79276	1722	succinate-CoA ligase, GDP-forming, beta subunit	4.34	down	0.00836
D90042_at	D90042	1767	N-acetyltransferase 2 (arylamine N-acetyltransferase)	3.79	down	0.00697
rc_F02028_at	F02028	1774	EST	3.15	down	0.00902
rc_F02245_at	F02245	1776	monoamine oxidase A	3.51	down	0.01692
rc_F03969_at	F03969	1785	matrix metalloproteinase 2 (gelatinase A, 72kD)	3.36	down	0.01685

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_H02855_at	H02855	1832	EST	4.29	down	0.0138
rc_H05704_s_at	H05704	1848	EST	3.07	down	0.00363
rc_H06935_s_at	H06935	1855	electron-transferring-flavoprotein dehydrogenase	4.04	down	0.01498
rc_H08102_at	H08102	1858	breast cell glutaminase	12.85	down	0.0424
rc_H09317_at	H09317	1864	EST	3.2	down	0.00914
rc_H10779_s_at	H10779		methylenetetrahydrofolate cyclohydrolase (NADP+ dependent), methenyltetrahydrofolate synthetase	3.09	down	0.0496
rc_H20543_at	H20543	1872	formyltetrahydrofolate synthetase	13.06	down	0.00218
rc_H27330_at	H27330	1897	DKFZP586B1621 protein	3.37	down	0.01318
rc_H29568_at	H29568	1909	EST	5	down	0.00426
rc_H55759_at	H55759	1914	EST	4.36	down	0.0398
rc_H57060_s_at	H57060	1949	EST	7.57	down	0.00875
rc_H57816_at	H57816	1954	EST	3.09	down	0.01327
rc_H58673_at	H58673	1957	EST	15.49	down	0.00002
rc_h58692_s_at	H58692	1960	formyltetrahydrofolate dehydrogenase	20.18	down	0.00485
rc_H59136_at	H59136	1962	EST	6.63	down	0.00033
rc_H62212_at	H62212	1969	telomeric repeat binding factor 2	3.23	down	0.00513
H66367_at	H66367	1977	EST	3.84	down	0.00133
rc_H66840_at	H66840	1978	EST	3.34	down	0.01884
rc_H77597_f_at	H77597	2000	metallothionein 1H	9.01	down	0.00022
			ficolin (collagen/fibrinogen domain-containing) 3 (Hakata antigen)	18.59	down	0
rc_H80901_s_at	H80901	2005		39.64	down	0.00002
rc_H81070_f_at	H81070	2006	RNA helicase-related protein	3.94	down	0.00123
rc_H87765_at	H87765	2017	KIAA0626 gene product	4.14	down	0.00058
H93246_s_at	H93246	2035	EST	8.62	down	0.01271
rc_H93381_at	H93381	2036	EST	3.91	down	0.00325
rc_H99727_at	H99727	2080	adipose differentiation-related protein; adipophilin	8.98	down	0.02071
HG1428-HT1428_s_at	HG1428-HT1428		hemoglobin, beta	3.81	down	0.01837
HG2379-HT3996_s_at	HG2379-HT3996		serine hydroxymethyltransferase 1 (soluble)	3.84	down	0.00795
HG2730-HT2827_s_at	HG2730-HT2827		fibrinogen, A alpha polypeptide			

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
HG2730-HT2828_s_at	HG2730-HT2828		fibrinogen, A alpha polypeptide	3.62	down	0.01013
HG2841-HT2968_s_at	HG2841-HT2968		albumin	4.62	down	0.00552
HG4533-HT4938_at	HG4533-HT4938	2088	protease inhibitor 4 (kallistatin)	3.35	down	0.01605
J02843_at	J02843		cytochrome P450, subfamily IIE (ethanol-inducible)	6.18	down	0.01308
J03810_at	J03810	2099	solute carrier family 2 (facilitated glucose transporter), member 2	3.6	down	0.02376
J03910_m1_at	J03910	2101	EST	18.13	down	0.00119
J04093_s_at	J04093	2106	UDP glycosyltransferase 1	3.28	down	0.02286
J04449_at	J04449	2110	cytochrome P450, subfamily IIIA (naphthidine oxidase), polypeptide 3	5.07	down	0.01733
J05158_at	J05158	2117	carboxypeptidase N, polypeptide 2, 83kD	3.37	down	0.01156
J05428_at	J05428	2120	UDP glycosyltransferase 2 family, polypeptide B7	4.86	down	0.03414
K02402_at	K02402	2125	coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia E)	6.64	down	0.04082
K02766_at	K02766	2126	complement component 9	5.03	down	0.0433
K03192_f_at	K03192	2127	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6	14.19	down	0.0307
K03192_f_at	K03192	2127	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6	8.02	down	0.03483
L00352_at	L00352	2131	low density lipoprotein receptor (familial hypercholesterolemia)	3.3	down	0.03487
L00389_f_at	L00389	2132	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2	3.87	down	0.00844
L04751_at	L04751	2138	cytochrome P450, subfamily IVA, polypeptide 11	8.13	down	0.02065
L05144_at	L05144	2139	phosphoenolpyruvate carboxykinase 1 (soluble) fatty-acid-Coenzyme A ligase, long-chain 1,fatty-acid-	4	down	0.021
L09229_s_at	L09229	2150	Coenzyme A ligase, long-chain 2	4.5	down	0.01347
L11931_at	L11931	2159	serine hydroxymethyltransferase 1 (soluble)	3.74	down	0.0056
L12760_s_at	L12760	2162	phosphoenolpyruvate carboxykinase 1 (soluble)	6.06	down	0.01005
L16883_s_at	L16883	2166	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9	5.85	down	0.04368

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
L21893_at	L21893	2176	solute carrier family 10 (sodium/bile acid cotransporter)	5.23	down	0.03367
L27050_at	L27050	2186	apolipoprotein F	4.18	down	0.04901
L32140_at	L32140	2192	afamin	5.39	down	0.02767
M10942_at	M10942	2233	metallothionein 1E (functional)	4.05	down	0.01412
M10943_at	M10943	2234	metallothionein 1F (functional)	6.23	down	0.00007
M13143_at	M13143	2249	kalikrein B plasma, (Fletcher factor) 1	3.04	down	0.008
M14777_s_at	M14777	2263	glutathione S-transferase A2,glutathione S-transferase A3	13.23	down	0.03224
M16594_at	M16594	2272	glutathione S-transferase A2	5.42	down	0.03813
M16750_s_at	M16750	2273	plim-1 oncogene	3.07	down	0.02391
M16974_s_at	M16974	2277	complement component 8, alpha polypeptide	10.85	down	0.02313
M25079_s_at	M25079	2305	hemoglobin, beta	4.31	down	0.01567
M26393_s_at	M26393	2309	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	4.3	down	0.02294
M29873_s_at	M29873	2318	cytochrome P450, subfamily IIIB (phenobarbital-inducible)	17.92	down	0.01469
M29874_s_at	M29874	2319	cytochrome P450, subfamily IIIB (phenobarbital-inducible)	8.13	down	0.01064
M30185_at	M30185	2321	cholesterol ester transfer protein, plasma	3.82	down	0.00131
M30185_at	M30185	2321	cholesterol ester transfer protein, plasma	3.31	down	0.00109
M31667_f_at	M31667	2331	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2	4.47	down	0.01116
M33317_f_at	M33317	2338	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7	11.47	down	0.02611
M34276_at	M34276	2341	plasminogen	3.08	down	0.02754
M57731_s_at	M57731	2359	GRO2 oncogene	3.16	down	0.02204
M61854_s_at	M61854	2370	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)	3.45	down	0.02849
M63967_at	M63967	2378	aldehyde dehydrogenase 5	3.88	down	0.00274
M68840_at	M68840	2388	monoamine oxidase A	3.1	down	0.01953

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
M68895_ma1_at	M68895	2390	alcohol dehydrogenase 6 (class V)	3.21	down	0.02095
M72885_ma1_s_at	M72885	2393	putative lymphocyte G0/G1 switch gene	3.34	down	0.02943
M76665_at	M76665	2398	hydroxysteroid (11-beta) dehydrogenase 1	6.06	down	0.01317
M81349_at	M81349	2405	serum amyloid A4, constitutive	10.97	down	0.01946
M83652_s_at	M83652	2408	properdin P factor, complement	6	down	0.00002
M83772_at	M83772	2409	flavin containing monooxygenase 3	5.14	down	0.02023
			insulin-like growth factor binding protein, acid labile			
M86826_at	M86826	2413	subunit	3.75	down	0.01157
M93405_at	M93405	2424	methylmalonate-semialdehyde dehydrogenase	3.09	down	0.03285
M94065_s_at	M94065	2425	dihydroorotate dehydrogenase	7.87	down	0.0011
M94065_at	M94065	2425	dihydroorotate dehydrogenase	3.61	down	0.00229
M95585_s_at	M95585	2430	hepatic leukemia factor	3.36	down	0.00492
			transducin-like enhancer of split 4, homolog of Drosophila			
M99439_at	M99439	2438	E(sp1)	4.82	down	0.00121
rc_N22404_at	N22404	2450	EST	3.44	down	0.02267
rc_N22938_s_at	N22938	2453	serum amyloid A4, constitutive	4.91	down	0.01918
			kyurenine 3-monoxygenase (kyurenine 3-hydroxylase)			
rc_N29353_at	N29353	2477	kyurenine 3-monoxygenase (kyurenine 3-hydroxylase)	3.44	down	0.01212
rc_N29764_at	N29764	2482	EST	4.48	down	0.0013
rc_N31741_at	N31741	2489	serine hydroxymethyltransferase 1 (soluble)	5.66	down	0.00212
rc_N34804_at	N34804	2497	DKFZP434J214 protein	3.97	down	0.0175
rc_N39163_at	N39163	2509	metallothionein 1L	4.3	down	0.03917
rc_N39201_at	N39201	2510	protease inhibitor 4 (kallistatin)	4.79	down	0.02015
rc_N49902_at	N49902	2540	EST	3.02	down	0.00951
rc_N51117_at	N51117	2544	EST	8.17	down	0.00105
rc_N51773_at	N51773	2549	EST	6.92	down	0.01839
			LIM protein (similar to rat protein kinase C-binding			
rc_N52271_at	N52271	2552	enigma)	3.67	down	0.01102
rc_N52322_at	N52322	2553	EST	4.58	down	0.02077
rc_N54053_at	N54053	2561	secreted phosphoprotein 2, 24kD	12.87	down	0.01821
rc_N54417_s_at	N54417	2567	fibrinogen, A alpha polypeptide	6.47	down	0.00733

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_N54429_at	N54429	2568	EST	6.85	down	0.03334
rc_N54950_s_at	N54950	2573	ketohexokinase (fructokinase)	6.47	down	0.0223
N57464_at	N57464	2576	CCAAT/enhancer binding protein (C/EBP), delta	4.87	down	0.00111
rc_N57934_s_at	N57934	2577	formiminotransferase cyclodeaminase	3.28	down	0.01555
rc_N58009_at	N58009	2578	formiminotransferase cyclodeaminase	8.52	down	0.01808
rc_N59550_at	N59550	2588	EST	4.78	down	0.02924
rc_N63391_at	N63391	2600	EST	3.87	down	0.02935
rc_N63845_at	N63845	2605	phytanoyl-CoA hydroxylase (Refsum disease) enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	6.82	down	0.00369
rc_N64036_s_at	N64036	2607	EST	6.12	down	0.00476
rc_N65959_at	N65959	2612	EST	3.38	down	0.00785
rc_N66066_at	N66066	2613	EST	4.33	down	0.0184
rc_N67105_at	N67105	2624	EST	4.69	down	0.00194
rc_N68596_s_at	N68596	2636	betaine-homocysteine methyltransferase	10.46	down	0.01971
rc_N70358_s_at	N70358	2657	growth hormone receptor solute carrier family 10 (sodium/bile acid cotransporter family), member 1	8.47	down	0.00816
rc_N70966_s_at	N70966	2663	EST	10.8	down	0.02894
rc_N73543_at	N73543	2675	EST	4.64	down	0.03981
rc_N74025_at	N74025	2685	deiodinase, iodothyronine, type I	8.18	down	0.01363
N77326_at	N77326	2696	EST	4.08	down	0.00768
rc_N80129_at	N80129	2703	metallothionein 1L	26.87	down	0.00999
rc_N80129_f_at	N80129	2703	metallothionein 1L	11.48	down	0.00167
rc_N90584_at	N90584	2714	EST	3.36	down	0.01561
N91087_at	N91087	2717	EST	3.66	down	0.00725
N99542_at	N99542	2747	orosomucoid 1	3.53	down	0.00607
rc_R01023_s_at	R01023	2752	glucokinase (hexokinase 4) regulatory protein	4.56	down	0.04036
rc_R08564_at	R08564	2780	plasminogen-like	8.77	down	0.01284
rc_R09053_at	R09053	2783	EST	3.45	down	0.03074
rc_R12472_at	R12472	2789	EST	12.09	down	0.02379
rc_R22905_at	R22905	2801	EST	4.31	down	0.01744
rc_R40395_s_at	R40395	2841	lactithin-cholesterol acyltransferase	12.85	down	0.01334

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Sq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_R40492_at	R40492	2842	EST	6.4	down	0.00527
rc_R40899_f_at	R40899	2844	glycine receptor, beta	4.84	down	0.02369
rc_R43799_at	R43799	2851	EST	3.93	down	0.005
rc_R49602_at	R49602	2885	EST	16.17	down	0.00279
rc_R59722_at	R59722	2916	EST	6.24	down	0.02361
rc_R65593_s_at	R65593	2935	kynureine 3-monooxygenase (kynureine 3-hydroxylase)	6.6	down	0.01982
rc_R66002_at	R66002	2936	EST	4.33	down	0.00789
R69417_at	R69417	2942	EST	6.43	down	0.00778
rc_R73816_at	R73816	2961	EST	7.05	down	0.01287
R77628_at	R77628	2966	insulin induced gene 1	5.51	down	0.0404
R79750_at	R79750	2971	EST	4.89	down	0.00695
R80048_at	R80048	2972	EST	3.61	down	0.01209
rc_R89811_s_at	R89811	2980	HGF activator	13.29	down	0.00148
rc_R92475_s_at	R92475	2987	flavin containing monooxygenase 3	6.46	down	0.02269
rc_R93714_at	R93714	2992	fetuin B	4.65	down	0.03704
R93776_s_at	R93776	2993	EST	5.55	down	0.00047
rc_R94674_s_at	R94674	2996	cytochrome P450, subfamily VIII B (sterol 12-alpha-hydroxylase), polypeptide 1	4.58	down	
rc_R97419_at	R97419	3004	hydroxylase)	19.3	down	0.000807
R98073_at	R98073	3009	EST	8.37	down	0.01436
rc_R99591_at	R99591	3016	CD5 antigen-like (scavenger receptor cysteine rich family) aldo-keto reductase family 1, member C4 (chlordeneone reductase; 3-alpha hydroxysteroid dehydrogenase, type I;	7.41	down	0.000043
S68287_at	S68287	3025	dihydrodiol dehydrogenase 4)	5.04	down	0.02895
S70004_at	S70004	3029	glycogen synthase 2 (liver)	5.13	down	0.00183
S77356_at	S77356	3034	EST	3.55	down	0.03874
rc_T10264_s_at	T10264	3051	EST	3.26	down	0.01718
rc_T16484_s_at	T16484	3071	EST	4.78	down	0.00009
rc_T40936_at	T40936	3118	EST	4.62	down	0.02844

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_T40995_f_at	T40995	3119	alcohol dehydrogenase 3 (class I), gamma polypeptide	3.42	down	0.00957
rc_T41047_s_at	T41047	3120	EST	3.08	down	0.00553
rc_T41232_at	T41232	3122	EST	3.14	down	0.02012
rc_T47778_s_at	T47778	3127	fibrinogen, A alpha polypeptide	3.33	down	0.00637
rc_T48075_f_at	T48075	3130	hemoglobin, alpha 1	35.75	down	0.00471
rc_T48278_at	T48278	3132	EST	24.1	down	0.00595
rc_T51150_at	T51150	3137	EST	8.65	down	0.00553
rc_T51617_at	T51617	3138	solute carrier family 22 (extraneuronal monoamine transporter), member 3	6.16	down	0.04198
rc_T52813_s_at	T52813	3142	putative lymphocyte G0/G1 switch gene	5.4	down	0.02021
rc_T56281_f_at	T56281	3151	RNA helicase-related protein	14.64	down	0.00027
T57140_s_at	T57140	3152	paraoxonase 3	8.47	down	0.01048
rc_T58756_at	T58756	3156	EST	16.61	down	
rc_T61256_s_at	T61256	3162	ketohexokinase (fructokinase)	3.56	down	0.04957
rc_T61649_f_at	T61649	3165	superoxide dismutase 2, mitochondrial	4.08	down	0.0389
rc_T63364_at	T63364	3170	ficolin (collagen/fibronectin domain-containing) 3 (Hakata antigen)	6.27	down	0.00455
rc_T64575_s_at	T64575	3172	EST	3.16	down	0.01855
rc_T67931_at	T67931	3184	fibrinogen, B beta polypeptide	17.25	down	0.00128
T68510_at	T68510	3187	EST	3.19	down	0.01504
rc_T68711_at	T68711	3188	EST	35.98	down	0.0003
rc_T68873_f_at	T68873	3190	metallothionein 1L	13.68	down	0.00593
rc_T68878_f_at	T68878	3191	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	4.18	down	0.02474
rc_T69305_at	T69305	3197	EST	15.87	down	0.02258
rc_T72502_at	T72502	3208	EST	4.74	down	0.00404
rc_T72906_at	T72906	3210	EST	4.91	down	0.00512
rc_T74542_s_at	T74542	3215	UDP glycosyltransferase 2 family, polypeptide B10	7.19	down	0.011
rc_T74608_at	T74608	3216	hydroxyl acid oxidase (glycolate oxidase) 1	6.1	down	0.00249
rc_T78433_s_at	T78433	3220	glycogen synthase 2 (liver)	5.74	down	0.00949
T83397_at	T83397	3233	phytanoyl-CoA hydroxylase (Refsum disease)	8.03	down	0.02173

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Sq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_T87174_at	T87174	3240	EST	3.46	down	0.00026
T95813_f_at	T95813	3262	KIAA1051 protein	20.36	down	0.01361
rc_T98199_L_at	T98199	3267	EST	4.05	down	0.00753
rc_T98676_at	T98676	3269	EST	11.15	down	0.0323
U02388_at	U02388	3278	cytochrome P450, subfamily IVF, polypeptide 2	4.4	down	0.00761
U06641_s_at	U06641	3287	UDP glycosyltransferase 2 family, polypeptide B15	6.37	down	0.01594
U08006_s_at	U08006	3290	complement component 8, alpha polypeptide	3.96	down	0.04272
U08021_at	U08021	3291	nicotinamide N-methyltransferase	3.63	down	0.03726
U20530_at	U20530	3322	secreted phosphoprotein 2, 24kD	5.31	down	0.01119
U21931_at	U21931	3326	fructose-bisphosphatase 1	3.17	down	0.0143
U22029_f_at	U22029	3327	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7	11.85	down	0.03538
U27699_at	U27699	3340	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12	3.65	down	0.00381
U50196_at	U50196	3377	adenosine kinase	3.03	down	0.00975
U50929_at	U50929	3380	betaine-homocysteine methyltransferase	8.04	down	0.0188
U51010_s_at	U51010	3381	nicotinamide N-methyltransferase	4.69	down	0.03099
U56814_at	U56814	3393	deoxyribonuclease I-like 3	17.69	down	0.00007
U56814_at	U56814	3393	deoxyribonuclease I-like 3	5.75	down	0.00152
U65932_at	U65932	3405	extracellular matrix protein 1	3.18	down	0.00575
U95090_at	U95090	3464	nephrosis 1, congenital, Finnish type (nephrin)	4.63	down	0.01595
W07723_at	W07723	3471	EST	3.51	down	0.00026
W26996_at	W26996	3484	EST	4.46	down	0.00734
W28414_at	W28414	3490	EST	4.06	down	0.00083
W28798_at	W28798	3492	phosphodiesterase 6A, cGMP-specific, rod, alpha	3.33	down	0.00222
W28944_at	W28944	3494	EST	6.9	down	0.01014
rc_W44745_at	W44745	3520	EST	3.87	down	0.01051
rc_W45560_at	W45560	3525	EST	3.48	down	0.0179
W55903_at	W55903	3546	adipose differentiation-related protein, adipophilin	5.64	down	0.00014
rc_W63728_at	W63728	3565	EST	3.86	down	0.00288
rc_W67147_at	W67147	3568	deleted in liver cancer 1	4.37	down	0.00069

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2:

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_W72044_at	W72044	3580	insulin induced gene 1 oxidative 3 alpha hydroxysteroid dehydrogenase; retinol dehydrogenase	3.1	down	0.03445
rc_W72382_at	W72382	3584		9.89	down	0.03091
rc_W73601_at	W73601	3592	EST	3.45	down	0.01382
rc_W73818_at	W73818	3593	EST	3.47	down	0.00927
rc_W81552_at	W81552	3615	EST	12.97	down	0.00244
rc_W86075_at	W86075	3624	EST	6.04	down	0.01486
rc_W86600_at	W86600	3628	EST	3.67	down	0.04208
rc_W87532_at	W87532	3634	putative glycine-N-acetyltransferase	5.5	down	0.00739
rc_W87781_at	W87781	3636	EST	4.02	down	0.00284
rc_W88946_at	W88946	3639	putative glycine-N-acetyltransferase	25.28	down	0.00221
rc_W95041_at	W95041	3662	EST	4.22	down	0.01005
X02176_s_at	X02176	3672	complement component 9	3.84	down	0.01793
X06562_at	X06562	3686	growth hormone receptor	4.8	down	0.00507
X06985_at	X06985	3689	heme oxygenase (decycling) 1	3.34	down	0.00045
X13227_at	X13227	3698	D-amino-acid oxidase	3.22	down	0.01753
X13930_f_at	X13930	3700	cytochrome P450, subfamily II A (phenobarbital-inducible), polypeptide 6	8.1	down	0.0219
X14813_at	X14813	3705	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3- oxoacyl-Coenzyme A thiolase)	3.53	down	0.00059
X16260_s_at	X16260	3710	inter-alpha (globulin) inhibitor, H1 polypeptide	3.76	down	0.00291
X16349_s_at	X16349	3712	sex hormone-binding globulin	6.61	down	0.00008
X54380_at	X54380	3730	pregnancy-zone protein	7.71	down	0.00069
X56411_mna1_at	X56411	3737	alcohol dehydrogenase 4 (class II), pi polypeptide	9.87	down	0.01416
X58022_at	X58022	3747	corticotroph releasing hormone-binding protein	4.09	down	0.00076
X63359_at	X63359	3759	UDP glycosyltransferase 2 family, polypeptide B10	4.26	down	0.01725
X64177_f_at	X64177	3763	metallothionein 1H	3.26	down	0.03928
X67491_f_at	X67491	3776	glutamate dehydrogenase 1	4.06	down	0.00273
X72177_mna1_at	X72177	3790	complement component 6	4.25	down	0.01598
X76717_at	X76717	3797	metallothionein 1L	5.64	down	0.00215
X90579_s_at	X90579	3819	EST	4.26	down	0.04759

Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
X95190_at	X95190	3832	acyl-Coenzyme A oxidase 2, branched chain	6.22	down	0.00162
X97324_at	X97324	3839	adipose differentiation-related protein; adipophilin	3.72	down	0.00202
Y00317_at	Y00317	3845	UDP glycosyltransferase 2 family, polypeptide B4'	4.63	down	0.02986
Z20777_at	Z20777	3866	EST	15.73	down	0.00147
Z28339_at	Z28339	3875	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	8.03	down	0.00853
Z31690_s_at	Z31690	3881	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	3.29	down	0.00161
rc_Z40259_s_at	Z40259	3919	EST	4.47	down	0.00093
rc_Z40305_at	Z40305	3920	EST	4.09	down	0.00096
rc_Z40902_at	Z40902	3926	SEC14 (S. cerevisiae)-like 2	4.97	down	0.04627
rc_Z41042_at	Z41042	3928	EST	3.37	down	0.00703
Z48475_at	Z48475	3943	glucokinase (hexokinase 4) regulatory protein	4.6	down	0.01693
			small inducible cytokine subfamily A (Cys-Cys), member			
Z49269_at	Z49269	3945	14	7.24	down	0.01047
Z69923_at	Z69923	3948	HGF activator	3.95	down	0.00012
Z80345_rna1_s_at	Z80345	3951	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	3.21	down	0.04734
Z84721_cds2_at	Z84721	3953	hemoglobin, zeta	7.39	down	0.01921

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA001504_f_at	AA001504	2	EST	4.44	up	0.03077
rc_AA005262_at	AA005262	13	EST KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing ARF-binding protein 2	3.09	up	0.0064
rc_AA007507_at	AA007507	18	CDC28 protein kinase 2	5.23	up	0.00159
rc_AA010065_s_at	AA010065	22	melanoma-associated antigen recognised by T	3.71	up	0.00432
rc_AA011209_s_at	AA011209	30	EST	6.45	up	0.00088
rc_AA011679_at	AA011679	32	EST	3.08	up	0.03649
rc_AA018346_at	AA018346	38	EST	3.69	up	0.04582
rc_AA021549_at	AA021549	42	EST	3.17	up	0.00158
rc_AA022623_at	AA022623	44	EST	3.27	up	0.01556
rc_AA024658_at	AA024658	47	ribosomal protein S19	7.55	up	0.00592
rc_AA024776_at	AA024776	48	EST	3.44	up	0.00334
rc_AA025166_s_at	AA025166	50	fusion, derived from t(12;16) malignant liposarcoma	3.17	up	0.00009
rc_AA026356_at	AA026356	57	EST	5.04	up	0.02483
rc_AA027833_l_at	AA027833	59	EST	5.02	up	0.01123
rc_AA029288_at	AA029288	65	EST	3.36	up	0.04908
rc_AA031814_at	AA031814	70	KIAA0958 protein	3.07	up	0.00681
rc_AA037058_s_at	AA037058	84	laminin, gamma 1 (formerly LAMB2)	4.11	up	0.02264
rc_AA037433_at	AA037433	86	EST	4.9	up	0.0194
rc_AA037766_at	AA037766	87	EST	3.63	up	0.0328
rc_AA040465_at	AA040465	95	EST	3.63	up	0.01806
rc_AA043111_s_at	AA043111	97	EST	6.36	up	0.00005
rc_AA043959_at	AA043959	101	tropomyosin 4	4.37	up	0.01641
rc_AA045365_at	AA045365	106	EST	3.17	up	0.0149
rc_AA046103_at	AA046103	109	EST	3.75	up	0.02893
rc_AA046410_s_at	AA046410	110	EST	3.18	up	0.00797
rc_AA046745_at	AA046745	113	Wolf-Hirschhorn syndrome candidate 1	3.33	up	0.00648
rc_AA047379_s_at	AA047379	119	Kanopherin (importin) beta 1	3.15	up	0.01572
rc_AA047704_at	AA047704	120	EST	3.2	up	0.00029
rc_AA052941_at	AA052941	121	EST	3.36	up	0.00088
rc_AA053662_f_at	AA053662	129	EST	3.3	up	0.00558

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA053680_at	AA053680	130	high-mobility group protein 2-like 1	4.07	up	0.03144
rc_AA055892_at	AA055892	134	EST	3.02	up	0.04984
rc_AA055896_at	AA055896	135	collagen, type V, alpha 1	10.87	up	0.00907
rc_AA070206_at	AA070206	155	EST	3.15	up	0.03914
rc_AA070485_at	AA070485	156	interleukin 13 receptor, alpha 1	3.19	up	0.03465
rc_AA070827_at	AA070827	157	EST	4.37	up	0.02617
AA071387_at	AA071387	158	jumping translocation breakpoint	3.31	up	0.0001
rc_AA074162_s_at	AA074162	159	superkiller viralicidic activity 2 (S. cerevisiae homolog)	3.23	up	0.00642
rc_AA076138_at	AA076138	167	H2A histone family, member Y	3.75	up	0.01442
AA086071_at	AA086071	184	chromosome-associated polypeptide C	3.77	up	0.01993
rc_AA086232_f_at	AA086232	186	Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))	4.52	up	0.00452
rc_AA086412_at	AA086412	187	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16	3.13	up	0.00327
AA089997_at	AA089997	189	EST	4.9	up	0.0241
AA091752_at	AA091752	193	purine-rich element binding protein B	3.25	up	0.01419
AA092129_f_at	AA092129	194	EST	5.67	up	0.00011
AA092290_f_at	AA092290	195	EST	3.25	up	0.01616
AA094752_at	AA094752	203	hypothetical 43.2 Kd protein	3.44	up	0.04445
rc_AA099404_s_at	AA099404	208	EST	20.22	up	0
rc_AA101272_at	AA101272	215	EST	3.83	up	0.0386
rc_AA102489_at	AA102489	219	EST	5.28	up	0.02122
rc_AA102837_f_at	AA102837	221	EST	4.13	up	0.0067
rc_AA112679_at	AA112679	224	EST	4.19	up	0.00572
rc_AA115562_at	AA115562	229	EST	3.35	up	0.00283
rc_AA115735_s_at	AA115735	230	EST	4.8	up	0.02671
rc_AA116036_at	AA116036	233	chromosome 20 open reading frame 1	3.41	up	0.00089
rc_AA122386_at	AA122386	239	collagen, type V, alpha 2	3.44	up	0.02566
rc_AA125808_at	AA125808	240	EST	3.04	up	0.02112
rc_AA127444_at	AA127444	252	EST	3.87	up	0.01751
rc_AA127741_at	AA127741	256	EST	4.49	up	0.0463

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
rc_AA128407_at	AA128407	259	EST	3.33	up	0.02298
rc_AA129757_at	AA129757	264	EST	3.75	up	0.0166
rc_AA131220_at	AA131220	267	EST	3.18	up	0.00974
rc_AA132032_s_at	AA132032	271	trinucleotide repeat containing 1	3.84	up	0.01136
rc_AA132514_at	AA132514	272	EST	3.2	up	0.00876
rc_AA133527_at	AA133527	281	EST	5.23	up	0.00037
rc_AA133666_s_at	AA133666	283	cysteine-rich protein 2	5.35	up	0.00433
rc_AA134052_s_at	AA134052	285	Rab geranylgeranyltransferase, alpha subunit	5.47	up	0.00982
rc_AA135153_at	AA135153	291	EST	5.58	up	0.00327
rc_AA135871_at	AA135871	294	EST	3.56	up	0.01718
rc_AA136269_at	AA136269	298	EST	7.5	up	0.00014
rc_AA136474_at	AA136474	301	Meis (mouse) homolog 2	3.15	up	0.02837
rc_AA136547_at	AA136547	302	EST	4.19	up	0.00098
rc_AA136864_at	AA136864	304	zinc finger protein homologous to Zfp-36 in mouse	3.31	up	0.00346
rc_AA142857_at	AA142857	307	EST	9.48	up	0.00376
rc_AA142858_at	AA142858	308	EST	4.07	up	0.0022
rc_AA146849_s_at	AA146849	313	target of myb1 (chicken) homolog	4.72	up	0.00326
rc_AA148885_at	AA148885	320	minichromosome maintenance deficient (S. cerevisiae) 4	6.59	up	0.00112
rc_AA148977_at	AA148977	322	EST	9.3	up	0.00002
rc_AA149889_at	AA149889	326	neighbor of A-kinase anchoring protein 95	8.55	up	0.00224
rc_AA151435_at	AA151435	336	EST	4.52	up	0.01134
rc_AA156187_at	AA156187	339	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit b, isoform 1	9.38	up	0.02007
rc_AA156460_at	AA156460	343	EST	4.39	up	0.01223
rc_AA159025_at	AA159025	353	EST	6.58	up	0.01946
rc_AA160775_s_at	AA160775	355	BCL2-antagonist of cell death	3.8	up	0.01145
rc_AA165526_at	AA165526	360	3-prime- phosphoadenosine 5-prime-phosphosulfate synthase 1	3.68	up	0.00021
rc_AA167708_at	AA167708	363	EST	3.19	up	0.01871
rc_AA171760_at	AA171760	367	EST	4.39	up	0.04582
rc_AA173430_at	AA173430	371	EST	3.74	up	0.01159

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
AA173505_at	AA173505	EST	3	up	0.01736
AA173597_at	AA173597	EST	3.37	up	0.03622
rc_AA173755_at	AA173755	EST	6.73	up	0.00666
rc_AA179787_at	AA179787	polyglutamine binding protein 1	4.71	up	0.00725
rc_AA179845_at	AA179845	EST	3.55	up	0.02484
rc_AA181580_s_at	AA181580	karyopherin (importin) beta 1	3.01	up	0.0125
rc_AA181705_f_at	AA181705	EST	5.9	up	0.00023
rc_AA182001_r_at	AA182001	EST	3.78	up	0.04446
AA187579_at	AA187579	MCT-1 protein	3.4	up	0.02455
rc_AA188378_i_at	AA188378	EST	4.88	up	0.01653
rc_AA194730_at	AA194730	EST	4.57	up	0.00801
rc_AA194998_at	AA194998	purinergic receptor (family A group 5)	3.06	up	0.04752
rc_AA195067_i_at	AA195067	GTPase activating protein-like	3.24	up	0.00606
rc_AA204927_at	AA204927	tropomyosin 1 (alpha)	6.11	up	0.0014
rc_AA207103_at	AA207103	EST	3.36	up	0.00131
rc_AA211483_at	AA211483	EST	4.11	up	0.0385
AA215299_s_at	AA215299	U6 snRNA-associated Sm-like protein LSm7	4.81	up	0.00119
rc_AA215379_at	AA215379	EST	4.44	up	0.01675
rc_AA218663_at	AA218663	acid-inducible phosphoprotein	4.34	up	0.00161
rc_AA226932_at	AA226932	DKFZP564F0923 protein	5.25	up	0.00612
rc_AA227145_at	AA227145	EST	3.4	up	0.03422
rc_AA227541_at	AA227541	NS1-binding protein	3.6	up	0.02801
AA232837_at	AA232837	EST	8.85	up	0.0048
rc_AA233897_at	AA233897	EST	3.8	up	0.02145
rc_AA234096_at	AA234096	EST	5.75	up	0.01169
rc_AA235289_at	AA235289	RAP2A, member of RAS oncogene family	4.31	up	0.00135
AA235448_s_at	AA235448	EST	5.62	up	0.00077
rc_AA235853_at	AA235853	CGI-96 protein	3.16	up	0.00744
rc_AA235868_at	AA235868	nuclear transcription factor Y, beta	3.49	up	0.01897
rc_AA236150_at	AA236150	3-prime-phosphoadenosine 5-prime-phosphosulfate synthase 1	3.46	up	0.0008
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Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
AA236412_at	AA236412	511	EST	3.1	up	0.04463
rc_AA236532_s_at	AA236532	513	EST	3.04	up	0.03747
rc_AA236672_at	AA236672	515	EST	4.37	up	0.00385
rc_AA236904_at	AA236904	518	EST	3.07	up	0.01503
rc_AA242757_at	AA242757	522	EST	3.27	up	0.00286
rc_AA243133_at	AA243133	525	serine/threonine kinase 15	7.03	up	0.00005
rc_AA243173_at	AA243173	526	EST	3.49	up	0.0401
AA249819_s_at	AA249819	535	EST	5.22	up	0.00049
rc_AA251230_at	AA251230	540	EST	3.25	up	0.01417
rc_AA251299_s_at	AA251299	541	KIAA0014 gene product	4.74	up	0.0252
rc_AA251428_at	AA251428	542	DKFZP586l2223 protein	3.15	up	0.01223
rc_AA251766_at	AA251766	543	EST	3.06	up	0.0098
rc_AA251769_at	AA251769	544	EST	4.45	up	0.01431
rc_AA251792_at	AA251792	546	fatty-acid-Coenzyme A ligase, long-chain 4	7.44	up	0.00285
rc_AA251909_at	AA251909	549	EST	3.59	up	0.01129
rc_AA252060_at	AA252060	550	EST	4.88	up	0.00169
rc_AA252355_at	AA252355	553	EST	3.02	up	0.00715
rc_AA252524_at	AA252524	555	EST	3.17	up	0.00686
chaperonin containing TCP1, subunit 6A (zeta 1),hemeo						
rc_AA252627_s_at	AA252627	556	box B5	4.28	up	0.00363
rc_AA253011_f_at	AA253011	558	KIAA0713 protein	3.15	up	0.00035
rc_AA255486_at	AA255486	568	EST	3.72	up	0.00154
rc_AA256131_at	AA256131	574	glycophosphatidylinositol anchor attachment 1	3.16	up	0.00011
rc_AA256268_at	AA256268	576	EST	3.13	up	0.03874
rc_AA256524_at	AA256524	580	AD022 protein	3.06	up	0.00626
rc_AA256606_at	AA256606	581	EST	3.92	up	0.03087
rc_AA256688_s_at	AA256688	584	EST	4.23	up	0.03094
rc_AA258131_at	AA258131	587	putative GTP-binding protein similar to RAY/RAB1C	6.23	up	0.00931
rc_AA258182_at	AA258182	589	EST	3.55	up	0.01198
rc_AA258387_at	AA258387	594	EST	3.15	up	0.02028
rc_AA258421_at	AA258421	595	hypothetical protein	6.5	up	0.00559

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA258614_s_at	AA258614	599	EST	3.94	up	0.0048
rc_AA262477_at	AA262477	608	ribonuclease HI, large subunit	4.57	up	0.00724
rc_AA262957_at	AA262957	612	EST	3.76	up	0.00157
AA263032_s_at	AA263032	614	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	6.73	up	0.04478
rc_AA278768_f_at	AA278768	617	EST	3.77	up	0.03239
rc_AA278817_at	AA278817	618	EST	3.5	up	0.01159
rc_AA279418_at	AA279418	626	EST	3.23	up	0.02054
rc_AA280734_l_at	AA280734	639	KIAA0618 gene product	6.83	up	0.001
rc_AA280840_at	AA280840	641	casein kinase 1, gamma 2	4.51	up	0.0186
rc_AA281599_at	AA281599	647	EST	4.87	up	0.00248
rc_AA282247_at	AA282247	657	EST	5.88	up	0.01112
rc_AA282343_at	AA282343	658	purine-rich element binding protein B	5.78	up	0.00128
rc_AA282571_at	AA282571	662	FSHD region gene 1	3.16	up	0.01355
rc_AA283182_at	AA283182	668	EST	6.78	up	0.01784
rc_AA283832_at	AA283832	672	EST	4.77	up	0.00156
rc_AA284565_f_at	AA284565	675	EST	3.27	up	0.0362
rc_AA284720_at	AA284720	676	EST	3.03	up	0.00252
rc_AA284945_at	AA284945	680	EST	6.25	up	0.0002
rc_AA285132_at	AA285132	682	apoptotic protease activating factor	3.1	up	0.00844
rc_AA286911_at	AA286911	684	EST	3.36	up	0.00037
rc_AA291137_at	AA291137	694	EST	3.67	up	0.03243
rc_AA291139_at	AA291139	695	EST	6.22	up	0.03491
rc_AA291168_at	AA291168	696	EST	4.93	up	0.01633
rc_AA291644_at	AA291644	701	EST	3.28	up	0.00033
rc_AA291659_at	AA291659	702	EST	4.15	up	0.00019
AA291786_s_at	AA291786	704	FE65-LIKE 2	4.15	up	0.00362
rc_AA292765_at	AA292765	712	ZW10 interactor	7.24	up	0.00498
rc_AA292788_s_at	AA292788	714	EST	3.65	up	0.01765
rc_AA293420_s_at	AA293420	717	EST	4.05	up	0.01189
rc_AA293589_s_at	AA293589	719	zinc finger protein	3.02	up	0.01809

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
AA293868_s_at	AA293868	721	EST	3.04	up	0.0054
AA296994_s_at	AA296994	724	seven transmembrane domain protein	3.16	up	0.0076
AA313213_at	AA313213	732	flotillin 1	3.59	up	0.00878
AA320369_s_at	AA320369	735	chromosome 19 open reading frame 3	3.88	up	0.00452
rc_AA321833_at	AA321833	736	EST	3.16	up	0.00523
rc_AA335191_f_at	AA335191	741	creatine kinase, brain	6.47	up	0.01462
rc_AA338760_at	AA338760	744	EST	3.96	up	0.01307
rc_AA365708_s_at	AA365708	764	microfibrillar-associated protein 1	3.01	up	0.02372
AA365742_s_at	AA365742	765	tetraspan NET-6 protein	4.12	up	0.00255
rc_AA370163_at	AA370163	766	EST	3.41	up	0.00134
AA384184_s_at	AA384184	774	DKFZP586B0519 protein	3.42	up	0.01222
AA393139_at	AA393139	775	geminin	7.44	up	0.00888
rc_AA394258_s_at	AA394258	779	RD RNA-binding protein	7.27	up	0.00054
rc_AA398141_at	AA398141	788	EST	3.3	up	0.00211
rc_AA398205_at	AA398205	789	EST	4.22	up	0.00059
rc_AA398563_at	AA398563	797	EST	3.14	up	0.01895
rc_AA398908_at	AA398908	801	EST	20.72	up	0.00114
rc_AA398926_f_at	AA398926	802	EST	8.25	up	0.00066
rc_AA399251_at	AA399251	804	EST	4.3	up	0.01578
rc_AA399264_at	AA399264	805	EST	3.51	up	0.00327
rc_AA400184_at	AA400184	809	KIAA0907 protein	4.11	up	0.01123
AA400643_s_at	AA400643	817	GAS2-related on chromosome 22	4.04	up	0.03751
rc_AA400896_at	AA400896	822	EST	3.54	up	0.00889
rc_AA401965_at	AA401965	833	tumor suppressor deleted in oral cancer-related 1	7.58	up	0.00089
rc_AA402272_at	AA402272	837	EST	3.73	up	0.02336
rc_AA402968_at	AA402968	844	EST	3.68	up	0.00123
O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosaminyl polypeptide-N-acetylglucosaminyl transferase)						
rc_AA404560_at	AA404560	853		3.73	up	0.0143
rc_AA405098_at	AA405098	855		6.09	up	0.01224
rc_AA405505_at	AA405505	860	RNA helicase family	4.05	up	0.00747

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA405544_f_at	AA405544	861	EST	3.09	up	0.04146
rc_AA405791_at	AA405791	864	EST	11.79	up	0.00587
rc_AA406216_at	AA406216	871	EST	3.4	up	0.00529
rc_AA406384_at	AA406384	875	KIAA0670 protein/actinus	3.23	up	0.00486
rc_AA410469_at	AA410469	883	EST	5.45	up	0.00068
rc_AA410962_s_at	AA410962	887	peroxisome proliferative activated receptor, delta	4.91	up	0.0044
rc_AA412301_at	AA412301	899	EST	3.42	up	0.0129
rc_AA412720_at	AA412720	905	EST	3.06	up	0.02153
rc_AA416970_at	AA416970	912	Mad4 homolog	5.3	up	0.00418
rc_AA416973_at	AA416973	913	EST	4.29	up	0.00155
rc_AA417030_at	AA417030	914	EST	7.35	up	0.00555
rc_AA417884_at	AA417884	919	cyclin-dependent kinase inhibitor-2C (p18, Inhibits	3.42	up	0.02997
AA421213_at	AA421213	931	Lsm3 protein	3.34	up	0.00198
rc_AA421562_at	AA421562	934	anterior gradient 2 (Xenopus laevis) homolog	5.02	up	0.02818
rc_AA421951_at	AA421951	936	EST	6.69	up	0.00013
rc_AA423827_f_at	AA423827	941	chromosome 22 open reading frame 3	4.39	up	0.00345
rc_AA423841_f_at	AA423841	942	EST	3.71	up	0.01481
rc_AA424029_at	AA424029	943	EST	4.54	up	0.02721
rc_AA424487_at	AA424487	945	EST	4.68	up	0.00113
rc_AA424881_at	AA424881	949	EST	3.39	up	0.03546
rc_AA425544_s_at	AA425544	955	eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD)	3.05	up	0.0346
rc_AA425852_s_at	AA425852	958	EST	3.98	up	0.02796
rc_AA425852_l_at	AA425852	958	EST	3.82	up	0.0395
rc_AA426291_at	AA426291	961	EST	3.03	up	0.00365
rc_AA426374_f_at	AA426374	964	tubulin, alpha 2	3.25	up	0.04346
rc_AA426447_at	AA426447	965	EST	3.01	up	0.02414
rc_AA426521_at	AA426521	967	Sjogren's syndrome nuclear autoantigen 1	3.33	up	0.01163
rc_AA427734_at	AA427734	977	cholinergic receptor, nicotinic, epsilon polypeptide	3.08	up	0.04796
AA428172_f_at	AA428172	986	Notch (Drosophila) homolog 3	9.63	up	0.00195

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA428204_at	AA428204	987	cofactor required for Sp1 transcriptional activation, subunit 6 (77kD)	3.08	up	0.00313
rc_AA429470_at	AA429470	996	EST	3.2	up	0.0153
rc_AA429472_at	AA429472	997	DKFZP434P106 protein	8.78	up	0.00063
AA429539_f_at	AA429539	999	EST	4.3	up	0.01035
rc_AA429572_at	AA429572	1000	ribosomal protein S6	3.31	up	0.02144
AA429825_at	AA429825	1003	DKFZP566B023 protein	3.11	up	0.01857
rc_AA430032_at	AA430032	1009	pitillary tumor-transforming 1	10.67	up	0.00052
rc_AA430048_at	AA430048	1012	KIAA0160 protein	4.32	up	0.00279
rc_AA430154_at	AA430154	1014	EST	3.09	up	0.04401
rc_AA430474_at	AA430474	1015	EST	4.69	up	0.00007
rc_AA430675_at	AA430675	1019	Fanconi anemia, complementation group G	3.16	up	0.01007
rc_AA431571_at	AA431571	1024	EST	4.62	up	0.0174
rc_AA431719_at	AA431719	1025	EST	3.19	up	0.00294
rc_AA433947_at	AA433947	1034	EST	3.09	up	0.00253
rc_AA434418_at	AA434418	1036	KIAA1115 protein	6.75	up	0.0032
rc_AA435662_f_at	AA435662	1039	EST	3.27	up	0.0433
rc_AA435665_at	AA435665	1040	EST	3.94	up	0.00274
rc_AA435681_s_at	AA435681	1041	EST	3.07	up	0.01166
rc_AA435748_at	AA435748	1044	EST	5.01	up	0.01812
rc_aa435769_s_at	AA435769	1046	EST	3.06	up	0.00615
AA442054_s_at	AA442054	1067	phospholipase C, gamma 1 (formerly subtype 148)	4.94	up	0.04102
rc_AA442155_at	AA442155	1068	transforming acidic collod-coll containing protein 3	3.35	up	0.00344
AA442400_at	AA442400	1071	hepatitis B virus x-interacting protein (9.6kD)	3.02	up	0.04037
rc_AA442763_at	AA442763	1072	cyclin B2	3.49	up	0.04176
rc_AA443271_at	AA443271	1073	KIAA0546 protein	3.44	up	0.00324
rc_AA443316_s_at	AA443316	1075	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	3.4	up	0.00133
rc_AA443602_at	AA443602	1078	EST	5.71	up	0.00736
rc_AA443802_at	AA443802	1081	EST	4.07	up	0.01546
rc_AA446242_at	AA446242	1087	EST	6.3	up	0.00169
rc_AA446570_at	AA446570	1089	EST	3.12	up	0.02228

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA446581_at	AA446581	1090	DKFZP564P0462 protein	4.04	up	0.00479
rc_AA446970_at	AA446970	1098	EST	3.09	up	0.01627
rc_AA447574_at	AA447574	1102	EST	4.12	up	0.00779
rc_AA448252_at	AA448252	1114	EST	3	up	0.00256
rc_aa449073_s_at	AA449073	1117	EST	5.61	up	0.01214
rc_aa449431_s_at	AA449431	1124	translation initiation factor IF2	3.76	up	0.00571
rc_AA449828_at	AA449828	1130	EST	3.35	up	0.01609
rc_AA450247_at	AA450247	1133	EST	3.13	up	0.00531
rc_AA451680_at	AA451680	1136	cancer associated gene 1	3.85	up	0.0018
rc_AA451877_at	AA451877	1138	EST	4.6	up	0.04045
AA451992_at	AA451992	1140	HSPC039 protein	3.33	up	0.01696
rc_AA452167_at	AA452167	1142	EST	3.29	up	0.03337
AA452724_at	AA452724	1149	programmed cell death 5	7.7	up	0.00085
rc_AA453628_at	AA453628	1154	EST	3.17	up	0.00849
rc_AA453656_at	AA453656	1155	EST	3.02	up	0.00958
rc_AA453783_s_at	AA453783	1158	EST	4.07	up	0.00786
rc_AA454597_s_at	AA454597	1166	EST	4.23	up	0.00917
rc_AA454830_at	AA454830	1170	DKFZP586M2123 protein	6.48	up	0.00555
AA454908_s_at	AA454908	1171	KIAA0144 gene product	6.39	up	0.01835
rc_AA455239_at	AA455239	1174	chromosome-associated polypeptide C	5.78	up	0.00003
rc_AA456415_at	AA456415	1192	KIAA0537 gene product	3.32	up	0.00155
rc_AA456583_s_at	AA456583	1193	PL6 protein	3.37	up	0.00139
rc_AA456646_at	AA456646	1196	EST	3.34	up	0.0309
rc_AA456852_at	AA456852	1199	suppressor of white apricot homolog 2	3.66	up	0.00614
rc_AA458878_s_at	AA458878	1204	EST	5.49	up	0.00977
rc_AA458890_at	AA458890	1206	EST	3.27	up	0.00078
rc_AA459254_at	AA459254	1211	EST	6.22	up	0.00001
AA459542_s_at	AA459542	1218	regulatory factor X-associated ankyrin-containing protein	3.4	up	0.00841
rc_AA460665_at	AA460665	1230	EST	4.01	up	0.01866
rc_aa460909_s_at	AA460909	1232	EST	5.02	up	0.01354

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA461063_at	AA461063	1235	EST	4.3	up	0.00074
AA461282_s_at	AA461282	1237	dihydropyrimidinase-like 2	3.42	up	0.02014
rc_AA461476_at	AA461476	1243	EST	3.72	up	0.00744
rc_AA463254_s_at	AA463254	1247	histone deacetylase 3	4.01	up	0.01858
rc_AA463934_at	AA463934	1253	splicing factor 3b, subunit 4, 49kD	3.15	up	0.00952
AA464043_s_at	AA464043	1255	EST	3.99	up	0.00056
rc_AA464251_at	AA464251	1257	EST	3.45	up	0.02229
rc_AA464414_1_at	AA464414	1258	EST	4.08	up	0.02299
rc_AA464423_at	AA464423	1259	EST	3.06	up	0.01416
rc_aa464722_s_at	AA464722	1263	DKFZP566C243 protein	3.51	up	0.00101
rc_AA464963_at	AA464963	1265	EST	4.77	up	0.00086
AA465000_s_at	AA465000	1266	EST	3.86	up	0.00431
rc_AA465093_at	AA465093	1267	TI1 cytototoxic granule-associated RNA-binding protein	3.3	up	0.01314
rc_AA465218_at	AA465218	1268	DKFZP586M1523 protein	3.17	up	0.00357
rc_AA465342_at	AA465342	1271	EST	3.21	up	0.01378
rc_AA470156_at	AA470156	1276	EST	4.99	up	0.0206
AA471384_at	AA471384	1278	divalent cation tolerant protein CUTA	3.44	up	0.01161
rc_AA476473_at	AA476473	1285	EST	3	up	0.01324
rc_AA476754_s_at	AA476754	1287	EST	3.18	up	0.01696
rc_AA476944_at	AA476944	1288	EST	3.29	up	0.00189
rc_AA477316_at	AA477316	1290	calumenin	3.05	up	0.00608
rc_AA477549_s_at	AA477549	1291	T-cell, immune regulator 1	4.84	up	0.04096
rc_AA478017_at	AA478017	1295	zyxin	4.25	up	0.01223
rc_AA478300_at	AA478300	1298	CD39-like 2	3.75	up	0.00152
rc_AA478415_at	AA478415	1299	EST	3.14	up	0.0483
rc_AA478422_at	AA478422	1301	unc-51 (C. elegans)-like kinase 1	3.83	up	0.00116
rc_AA478615_s_at	AA478615	1305	H1 histone family, member X	3.09	up	0.0499
			disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)	3.25	up	0.02698
rc_AA479096_at	AA479096	1308	EST	3.32	up	0.00118
rc_AA479139_s_at	AA479139	1310	acid phosphatase 1, soluble	3.42	up	0.01853

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA479881_at	AA479881	1317	EST	3.34	up	0.03289
rc_AA481060_at	AA481060	1326	EST	3.08	up	0.00029
rc_AA481420_at	AA481420	1327	EST	3.08	up	0.0206
rc_AA482104_s_at	AA482104	1332	non-metastatic cells 3, protein expressed in	4.78	up	0.00135
rc_AA482224_f_at	AA482224	1334	putative type II membrane protein	4.47	up	0.0001
AA482319_f_at	AA482319	1335	putative type II membrane protein	4.9	up	0.00028
AA482319_i_at	AA482319	1335	putative type II membrane protein	3.13	up	0.00071
rc_AA485060_at	AA485060	1339	EST	3.83	up	0.03172
rc_AA485084_s_at	AA485084	1340	EST	3.31	up	0.01232
rc_AA48531_s_at	AA48531	1345	EST	3.81	up	0.00441
rc_AA485697_at	AA485697	1346	EST	3.53	up	0.03566
rc_AA487218_at	AA487218	1355	EST	4.43	up	0.03198
rc_AA487856_at	AA487856	1359	KIAA0676 protein	3.59	up	0.01408
rc_AA488074_at	AA488074	1360	cell division cycle 42 (GTP-binding protein, 25kD)	3.74	up	0.01887
rc_AA48832_at	AA488432	1361	phosphoserine phosphatase	4.2	up	0.00128
rc_AA488872_s_at	AA488872	1363	EST	3.35	up	0.03191
rc_AA488892_at	AA488892	1364	EST	4.14	up	0.04766
rc_AA488901_at	AA488901	1368	EST	3.58	up	0.0002
rc_AA489707_at	AA489707	1371	EST	3.5	up	0.03208
rc_AA489712_at	AA489712	1372	EST	4.69	up	0.00587
rc_AA490212_at	AA490212	1375	H2A histone family, member Y solute carrier family 2 (facilitated glucose transporter),	3.52	up	0.02202
AA491188_at	AA491188	1387	member 3	5.04	up	0.02291
rc_AA491295_at	AA491295	1390	calcium/calmodulin-dependent protein kinase kinase 2,	3.71	up	0.0103
AA495857_at	AA495857	1394	EST	3.21	up	0.02243
rc_AA496715_f_at	AA496715	1400	spectrin SH3 domain binding protein 1	3.44	up	0.00069
rc_AA496981_at	AA496981	1404	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3	5.82	up	0.00521
rc_AA497018_at	AA497018	1406	adenylyl cyclase 1 (brain)	4.81	up	0.00352
AA504413_at	AA504413	1413	EST	3.31	up	0.00036
rc_AA504512_s_at	AA504512	1415	KIAA0943 protein	5.72	up	0.00384

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA505133_at	AA505133	1417	solute carrier family 2 (facilitated glucose transporter), member 3	12.21	up	0.00169
rc_AA505141_at	AA505141	1418	EST	3.08	up	0.02327
rc_AA521149_at	AA521149	1420	EST	3.33	up	0.00211
rc_AA598405_at	AA598405	1424	membrane interacting protein of RGS16	3.87	up	0.00649
rc_AA598447_at	AA598447	1428	exportin, tRNA (nuclear export receptor for tRNAs)	3.5	up	0.01201
rc_AA598589_at	AA598589	1431	EST	3.24	up	0.00432
rc_AA598648_s_at	AA598648	1432	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	3.46	up	0.00293
rc_AA598712_at	AA598712	1436	EST	3.45	up	0.00005
rc_AA598749_at	AA598749	1438	EST	3.01	up	0.03714
rc_AA598829_s_at	AA598829	1439	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	3.04	up	0.00967
rc_AA598831_f_at	AA598831	1440	EST	3.41	up	0.00452
rc_AA599469_at	AA599469	1450	EST	3.07	up	0.04154
rc_AA599808_at	AA599808	1455	EST	3.09	up	0.00726
rc_AA599850_at	AA599850	1457	EST	3.55	up	0.03215
rc_AA600153_at	AA600153	1460	DEK oncogene (DNA binding)	3.71	up	0.02967
rc_AA608668_at	AA608668	1465	erythrocyte membrane protein band 4.1-like 2	3.33	up	0.02014
rc_AA608897_at	AA608897	1473	EST	5.05	up	0.01782
rc_AA609008_at	AA609008	1475	EST	4.04	up	0.00002
rc_AA609080_at	AA609080	1478	EST	3.71	up	0.0306
rc_AA610073_at	AA610073	1497	EST	3.25	up	0.00859
rc_AA610089_at	AA610089	1498	U4/U6-associated RNA splicing factor	4.07	up	0.00361
rc_AA610116_1_at	AA610116	1499	tetraspan NET-6 protein	16.35	up	0.00249
rc_AA620461_at	AA620461	1501	EST	3.45	up	0.01146
rc_AA620553_s_at	AA620553	1504	flap structure-specific endonuclease 1	7.56	up	0.00101
rc_AA620761_at	AA620761	1507	EST	3.3	up	0.00285
rc_AA620779_at	AA620779	1508	golgin-67	3.35	up	0.00297
rc_AA620881_at	AA620881	1510	trinucleotide repeat containing 3	9.49	up	0.00062
rc_AA621146_at	AA621146	1514	MUF1 protein	3.15	up	0.02116

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_AA621242_s_at	AA621242	1518	hypothetical protein,peptidylprolyl isomerase B	4.59	up	0.00081
rc_AA621367_at	AA621367	1523	EST	3.1	up	0.00066
rc_AA621409_at	AA621409	1524	putative type II membrane protein	3.5	up	0.00462
rc_AA621530_at	AA621530	1526	EST	3.26	up	0.00298
rc_AA621535_at	AA621535	1527	FE65-LIKE 2	3.37	up	0.0167
rc_AA621752_at	AA621752	1529	26S proteasome-associated p41 homolog	3.13	up	0.01571
AB002373_at	AB002373	1538	KIAA0375 gene product	4.41	up	0.00795
AF003521_at	AF003521	1545	Jagged 2	3.58	up	0.00299
AF004022_at	AF004022	1546	serine/threonine kinase 12	3.29	up	0.00841
C00358_at	C00358	1552	nucleolar protein 3 (apoptosis repressor with CARD	3.45	up	0.00985
C01721_at	C01721	1558	phospholipase C, beta 3, neighbor pseudogene	5.89	up	0.0383
C01766_s_at	C01766	1559	EST	8.18	up	0.00505
rc_C14051_f_at	C14051	1565	phosphoprotein enriched in astrocytes 15	4.79	up	0.00548
rc_C14098_f_at	C14098	1566	EST	4.62	up	0.01654
rc_C14756_f_at	C14756	1570	MLN51 protein	3.75	up	0.0226
rc_C14835_f_at	C14835	1571	EST	3.35	up	0.0316
D00596_at	D00596	1590	thymidylate synthetase	5.58	up	0.0098
D133370_at	D133370	1603	APEX nuclease (multifunctional DNA repair enzyme)	3.07	up	0.00857
D13636_at	D13636	1606	general transcription factor IIIc, polypeptide 2 (beta subunit, 110kD)	3.12	up	0.00022
D13640_at	D13640	1608	KIAA0015 gene product	3.55	up	0.00347
D14657_at	D14657	1615	KIAA0101 gene product	3.84	up	0.02048
rc_D20899_at	D20899	1626	EST	3.13	up	0.02128
D21063_at	D21063	1628	minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin)	3.25	up	0.03558
D26129_at	D26129	1635	ribonuclease, RNase A family, 1 (pancreatic)	6.9	up	0.00008
D28589_at	D28589	1637	EST	3.38	up	0.01144
D30946_at	D30946	1638	kinesin family member 3B	3.43	up	0.01458
D31094_at	D31094	1639	G8 protein	9.37	up	0.0048
D31294_at	D31294	1643	EST	3.3	up	0.004
D31417_at	D31417	1645	secreted protein of unknown function	3.69	up	0.0004

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
D38073_at	D38073	1651	minichromosome maintenance deficient (<i>S. cerevisiae</i>) 3	4.1	up	0.01195
D38305_at	D38305	1652	transducer of ERBB2, 1	3.22	up	0.0215
D42040_s_at	D42040	1657	female sterile homeotic-related gene 1 (mouse homolog)	4.02	up	0.00389
rc_D51072_s_at	D51072	1674	biliverdin reductase A	3.34	up	0.0254
rc_D51276_f_at	D51276	1678	leukemia-associated phosphoprotein p18 (stathmin)	9.42	up	0.00015
D55716_at	D55716	1686	minichromosome maintenance deficient (<i>S. cerevisiae</i>) 7	5.48	up	0.00003
rc_D57317_at	D57317	1688	activated RNA polymerase II transcription cofactor 4	3.17	up	0.00464
rc_D59355_s_at	D59355	1696	cytoskeleton-associated protein 1	6.05	up	0.0015
rc_D59553_f_at	D59553	1697	golgin-67	5.95	up	0.00169
rc_D59570_f_at	D59570	1699	EST	4.34	up	0.00487
rc_D60811_s_at	D60811	1704	EST	4.34	up	0.00217
D63478_at	D63478	1711	KIAA0144 gene product	3.89	up	0.00253
D63486_at	D63486	1712	KIAA0152 gene product	3.56	up	0.00063
rc_D80420_at	D80420	1732	ubiquinol-cytochrome c reductase hinge protein	3.86	up	0.00412
rc_D80710_f_at	D80710	1734	Integral type I protein	3.17	up	0.04549
rc_D80917_f_at	D80917	1736	KIAA0670 protein/actinus	3.09	up	0.00168
rc_D80946_f_at	D80946	1737	SFRS protein kinase 1	3.07	up	0.00986
D81608_at	D81608	1740	polymerase (RNA) II (DNA directed) polypeptide K	3.52	up	0.00437
D82226_s_at	D82226	1742	proteasome (prosome, macropain) 26S subunit,	4.35	up	0.00184
D82277_s_at	D82277	1743	LDL induced EC protein	3.33	up	0.00355
D82558_at	D82558	1746	novel centrosomal protein RanBPM	4.67	up	0.00458
			trinucleotide repeat containing 11 (THR-associated protein, 230 kDa subunit)			
D83783_at	D83783	1748		4.16	up	0.00055
D84557_at	D84557	1749	minichromosome maintenance deficient (<i>mls5, S.</i>	3.97	up	0.0017
D86957_at	D86957	1754	KIAA0202 protein	3.08	up	0.02949
D86977_at	D86977	1757	KIAA0224 gene product	3.03	up	0.00053
rc_F01538_s_at	F01538	1771	RAP1, GTPase activating protein 1	4.88	up	0.00292
rc_F01568_at	F01568	1772	EST	4.13	up	0.00084
rc_F01831_at	F01831	1773	EST	5.95	up	0.00532
rc_F02254_s_at	F02254	1777	Fas-activated serine/threonine kinase	5.1	up	0.00329
rc_F02807_at	F02807	1781	KIAA0838 protein	5.67	up	0.02064

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_F02863_at	F02863	1782	EST	3.05	up	0.03504
rc_F04320_s_at	F04320	1786	replication factor C (activator 1) 4 (37kD)	6.29	up	0.00042
rc_F04444_at	F04444	1788	EST	4.13	up	0.00944
rc_F04479_at	F04479	1789	KIAA1067 protein	3.23	up	0.04522
rc_F08876_at	F08876	1797	EST	9.06	up	0
rc_F09788_at	F09788	1808	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	3.67	up	0.01682
rc_F10199_f_at	F10199	1813	EST	3.93	up	0.03209
rc_F10290_at	F10290	1815	EST	3.39	up	0.02392
rc_F10453_at	F10453	1819	EST	3.64	up	0.01878
rc_F10741_at	F10741	1822	KIAA0622 protein	3.01	up	0.03079
rc_F13809_f_at	F13809	1828	tropomyosin 1 (alpha)	4.4	up	0.01221
rc_H00540_at	H00540	1829	EST	3.74	up	0.00234
rc_H05084_at	H05084	1844	EST	5.85	up	0.00559
rc_H07873_at	H07873	1856	EST	3.53	up	0.0391
rc_H08863_at	H08863	1859	hypothetical protein	7.18	up	0.02102
rc_H09241_s_at	H09241	1861	EST	3.05	up	0.01487
rc_H09271_f_at	H09271	1862	EST	4.78	up	0.00072
rc_H10933_at	H10933	1873	EST	6.18	up	0.00003
rc_H11320_s_at	H11320	1875	SUMO-1 activating enzyme subunit 2	3.06	up	0.00167
rc_H16251_s_at	H16251	1886	EST	3.3	up	0.03286
rc_H27188_f_at	H27188	1908	collagen-binding protein 2 (collagen 2)	5.84	up	0.01826
rc_H27897_s_at	H27897	1911	hypothetical protein	3.01	up	0.00174
rc_H28333_f_at	H28333	1912	melanoma adhesion molecule	4.94	up	0.00166
rc_H41529_at	H41529	1926	EST	5.06	up	0.03309
H46486_s_at	H46486	1932	nesca protein	4.57	up	0.00749
rc_H47357_f_at	H47357	1934	EST	3.65	up	0.03789
rc_H48459_s_at	H48459	1937	KIAA0186 gene product	3.1	up	0.02325
rc_H52937_at	H52937	1944	roundabout (axon guidance receptor, Drosophila)	4.02	up	0.00163
rc_H56345_f_at	H56345	1950	EST	3.73	up	0.00853
rc_H57709_s_at	H57709	1956	ribosomal protein L31	4.41	up	0.00091

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_H59617_at	H59617	1964	EST	5.81	up	0.0115
rc_H62474_f_at	H62474	1970	EST	3.39	up	0.04173
rc_H64493_f_at	H64493	1973	immunoglobulin heavy constant gamma 3 (G3m marker) phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	4.74	up	0.00751
rc_H65030_s_at	H65030	1974		3.26	up	0.02278
rc_H65042_at	H65042	1975	EST	3.44	up	0.0006
rc_H67964_at	H67964	1981	EST	3.06	up	0.02707
rc_H68794_at	H68794	1984	EST	3.67	up	0.00327
rc_H70739_f_at	H70739	1991	EST	4.34	up	0.00106
rc_H73484_s_at	H73484	1995	ferritin, heavy polypeptide 1	3.18	up	0.00432
rc_H78211_at	H78211	2001	EST	7.5	up	0.02674
rc_H86072_f_at	H86072	2015	EST	4.49	up	0.01301
rc_H88674_s_at	H88674	2021	collagen, type I, alpha 2	4.15	up	0.02664
rc_H89987_s_at	H89987	2027	ATP-binding cassette, sub-family C (CFTR/MRP),	3.13	up	0.01194
rc_H91632_at	H91632	2031	EST	3.5	up	0.03688
rc_H94471_at	H94471	2042	occludin	6.26	up	0.00379
rc_H96850_at	H96850	2055	dolichyl-diphosphooligosaccharide-protein	3.03	up	0.00679
rc_H97012_at	H97012	2058	EST	3.51	up	0.03505
rc_H97013_at	H97013	2059	ephrin-A4	6.8	up	0.00023
rc_H97677_s_at	H97677	2062	EST	4.34	up	0.00753
rc_H99261_s_at	H99261	2074	EST	3.33	up	0.00319
rc_H99364_at	H99364	2075	chloride channel 7	3.03	up	0.01727
rc_H99473_s_at	H99473	2077	regulator of nonsense transcripts 1	6.51	up	0.00025
rc_H99489_s_at	H99489	2078	quiescin Q6	3.4	up	0.02682
rc_H99587_s_at	H99587	2079	EST	4.44	up	0.00532
rc_H99774_at	H99774	2081	EST	3.51	up	0.00008
rc_H99877_at	H99877	2083	exportin, tRNA (nuclear export receptor for tRNAs)	3.75	up	0.00302
rc_H99879_at	H99879	2084	EST	10.81	up	0.001

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
J00231_f_at	J00231	2087	immunoglobulin heavy constant gamma 3 (G3m marker)	6.23	up	0.00177
J03040_at	J03040	2091	secreted protein, acidic, cysteine-rich (osteonectin)	3.77	up	0.00594
J03464_s_at	J03464	2094	collagen, type I, alpha 2	10.37	up	0.00979
J04029_s_at	J04029	2102	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	3.02	up	0.00032
J05614_at	J05614	2122	EST	3.73	up	0.03419
L03411_s_at	L03411	2134	RD RNA-binding protein	4.06	up	0.00467
L04270_at	L04270	2135	lymphotoxin beta receptor (TNFR superfamily, member 3.5	up	0.01547	
L06797_s_at	L06797	2143	chemokine (C-X-C motif), receptor 4 (fusin)	3.23	up	0.04782
L11669_at	L11669	2157	tetracycline transporter-like protein	3.4	up	0.02062
L17131_ma1_at	L17131	2168	high-mobility group (nonhistone chromosomal) protein isoforms I and Y	4.45	up	0.03141
L25444_at	L25444	2181	TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD	3.78	up	0.00011
L26876_at	L26876	2182	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	4.43	up	0.00082
L28821_at	L28821	2188	mannosidase, alpha, class 2A, member 2	4.63	up	0.00876
L29218_s_at	L29218	2190	CDC-like kinase 2	6.51	up	0.00019
L29218_at	L29218	2190	CDC-like kinase 2	3.82	up	0.00035
L33930_s_at	L33930	2198	CD24 antigen (small cell lung carcinoma cluster 4 transcription elongation factor B (SIII), polypeptide 1	4.35	up	0.03968
L34587_at	L34587	2200	(15kD, elongin C)	3.12	up	0.00946
L47125_s_at	L47125	2218	glypican 3	10.69	up	0.04129
L76191_at	L76191	2222	interleukin-1 receptor-associated kinase 1	3.85	up	0.00152
L76568_xpt3_f_at	L76568	2225	excision repair cross-complementing rodent repair deficiency, complementation group 4	3.4	up	0.0172
M12125_at	M12125	2241	tropomyosin 2 (beta)	7.13	up	0.0004
M14483_ma1_s_at	M14483	2261	prothymosin, alpha (gene sequence 28)	3.36	up	0.00033
M19267_s_at	M19267	2286	tropomyosin 1 (alpha)	4.3	up	0.00893

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
M21259_at	M21259	2293	small nuclear ribonucleoprotein polypeptide E	3.68	up	0.00415
M26576_cds2_at	M26576	2310	EST	3.48	up	0.00062
AFFX-M27830_5_at	M27830	2314	EST	4.6	up	0.04719
AFFX-M27830_M_at	M27830	2314	EST	3.54	up	0.00777
AFFX-M27830_5_at	M27830	2314	EST	3.3	up	0.02453
M31303_ma1_at	M31303	2327	leukemia-associated phosphoprotein p18 (stathmin)	5.86	up	0.00071
M32977_s_at	M32977	2336	vascular endothelial growth factor v-erb-b2 avian erythroblastic leukemia viral oncogene	3.93	up	0.04917
M34309_at	M34309	2342	homolog 3	3.49	up	0.00191
M35252_at	M35252	2343	transmembrane 4 superfamily member 3	4.65	up	0.04128
M37583_at	M37583	2349	H2A histone family, member Z	4.25	up	0.00135
M55210_at	M55210	2353	laminin, gamma 1 (formerly LAMB2)	3.47	up	0.02551
M55998_s_at	M55998	2356	collagen, type I, alpha 1	3.54	up	0.01449
M57710_at	M57710	2357	lectin, galactoside-binding, soluble, 3 (galectin 3)	6.76	up	0.00103
M57730_at	M57730	2358	ephrin-A1	3.39	up	0.00199
M60784_s_at	M60784	2366	small nuclear ribonucleoprotein polypeptide A	4.74	up	0.00001
M61916_at	M61916	2372	laminin, beta 1	3.18	up	0.01171
M63573_at	M63573	2377	peptidylprolyl isomerase B (cyclophilin B)	3.59	up	0.00916
M68864_at	M68864	2389	ORF	3.95	up	0.00144
M86667_at	M86667	2411	nucleosome assembly protein 1-like 1 stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	3.08	up	0.00473
M86752_at	M86752	2412	replication factor C (activator 1) 4 (37kD)	5.15	up	0.02881
M87339_at	M87339	2415	chromosome 11 open reading frame 13	4.59	up	0.00116
M91083_at	M91083	2419	membrane component, chromosomal 4, surface marker (35kD glycoprotein)	3.19	up	0.00243
M93036_at	M93036	2422	midkine (neurite growth-promoting factor 2)	3.07	up	0.04189
M94250_at	M94250	2426	capping protein (actin filament), gelsolin-like	9.86	up	0.02104
M94345_at	M94345	2427	nuclear autoantigenic sperm protein (histone-binding)	3.59	up	0.04508
M97856_at	M97856	2436	EST	3.21	up	0.00444
rc_N21407_at	N21407	2443	MpV17 transgene, murine homolog, glomerulosclerosis	3.47	up	0.01037
rc_N21648_s_at	N21648	2447	up	0.00071		

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_N26904_at	N26904	2469	EST	15.38	up	0.00077
rc_N29484_at	N29484	2478	EST	3.08	up	0.04834
rc_N29742_at	N29742	2481	EST	3.74	up	0.00104
rc_N31597_s_at	N31597	2487	DKFZP564G2022 protein	3.17	up	0.03017
rc_N33920_at	N33920	2493	dubiquitin	50.29	up	0
rc_N34825_s_at	N34825	2498	DKFZP434P106 protein	3.27	up	0.01334
rc_N35913_at	N35913	2503	EST	3.48	up	0.0016
N36432_at	N36432	2507	erythrocyte membrane protein band 4.1-like 2	7.95	up	0.00067
rc_N39237_at	N39237	2511	EST	3.45	up	0.02481
N42272_s_at	N42272	2515	EST	3.03	up	0.0017
			eukaryotic translation Initiation factor 3, subunit 3			
rc_N47956_at	N47956	2524	(gamma, 40kD)	3.76	up	0.00968
rc_N48790_at	N48790	2532	EST	3.32	up	0.00654
rc_N51590_s_at	N51590	2546	EST	3.01	up	0.04345
rc_N51771_at	N51771	2548	KIAA0652 gene product	3.5	up	0.00028
			ADP-ribosyltransferase (NAD+; poly (ADP-ribose))			
rc_N51855_at	N51855	2550	polymerase)-like 3	3.39	up	0.00115
rc_N52168_at	N52168	2551	EST	3.66	up	0.00127
rc_N53067_at	N53067	2557	DKFZP547E1010 protein	3.1	up	0.00101
rc_N54067_at	N54067	2562	mitogen-activated protein kinase kinase kinase 4	4.82	up	0.00229
rc_N54841_at	N54841	2572	EST	5.87	up	0.02752
rc_N56935_s_at	N56935	2575	EST	4.04	up	0.00797
rc_N59536_at	N59536	2586	EST	11.68	up	0.00484
rc_N62126_at	N62126	2589	EST	6.42	up	0.00109
rc_N64374_at	N64374	2608	KIAA0537 gene product	3.25	up	0.01652
rc_N67815_f_at	N67815	2627	EST	3.84	up	0.00439
rc_N68018_at	N68018	2631	TBP-associated factor 172	3.84	up	0.00277
rc_N68241_at	N68241	2634	EST	4.32	up	0.00532
rc_N69084_i_at	N69084	2643	EST	3.11	up	0.0084
rc_N69252_f_at	N69252	2647	ferritin, light polypeptide	3.69	up	0.04116
rc_N69263_at	N69263	2648	EST	5.26	up	0.0276

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_N69390_at	N69390	2650	EST	3.99	up	0.00016
rc_N69879_s_at	N69879	2651	drebrin 1	3.15	up	0.01659
rc_N70481_at	N70481	2658	EST	4.13	up	0.0099
rc_N70678_s_at	N70678	2660	TAR (HIV) RNA-binding protein 1 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	3.78	up	0.02858
rc_N72116_s_at	N72116	2668	EST	5.57	up	0.00709
rc_N73705_at	N73705	2677	EST	3.75	up	0.01762
rc_N73762_f_at	N73762	2678	EST	3.67	up	0.00796
rc_N73808_f_at	N73808	2679	EST	6.44	up	0.00352
rc_N73865_at	N73865	2681	EST	4.43	up	0.00177
rc_N75541_at	N75541	2692	EST	4.43	up	0.01059
rc_N80703_at	N80703	2704	EST	5.65	up	0.0001
rc_N90238_l_at	N90238	2712	EST	3.13	up	0.02492
rc_N91773_at	N91773	2719	lysyl oxidase	4.31	up	0.00302
rc_N92948_s_at	N92948	2726	nuclear phosphoprotein similar to <i>S. cerevisiae</i> PW1	4.09	up	0.0019
rc_N93299_f_at	N93299	2732	nuclear receptor co-repressor 1	6.99	up	0.0371
rc_N93316_at	N93316	2733	EST	3.16	up	0.01262
rc_N93798_at	N93798	2738	protein tyrosine phosphatase type IV A, member 3	4.91	up	0.00245
rc_N98464_s_at	N98464	2744	EST	3.68	up	0.03007
rc_N98758_f_at	N98758	2745	EST	3.54	up	0.02609
rc_N9944_s_at	N9944	2749	EST	3.46	up	0.00104
rc_R05316_s_at	R05316	2760	EST	4.2	up	0.00011
rc_R06251_f_at	R06251	2764	tumor protein D52-like 2	4.88	up	0.03097
rc_R06254_f_at	R06254	2765	tumor protein D52-like 2	3.53	up	0.04865
rc_R06400_at	R06400	2768	EST	3.03	up	0.03266
rc_R06986_f_at	R06986	2776	peptidylprolyl isomerase B (cyclophilin B)	7.03	up	0.00628
rc_R07172_l_at	R07172	2777	EST	5.54	up	0.01322
rc_R15740_at	R15740	2791	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	3.36	up	0.00268
rc_R16144_at	R16144	2794	EST	3.24	up	0.0087
rc_R20817_s_at	R20817	2797	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	3.03	up	0.01091
rc_R22565_at	R22565	2800	EST	3.52	up	0.04352

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
				3.8	up	0.00266
rc_R26744_at	R26744	2804	midline 1 (Opitz/BBB syndrome)	3.53	up	0.03056
rc_R27016_s_at	R27016	2806	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)	3.41	up	0.00309
rc_R27296_f_at	R27296	2807	EST			
rc_R28636_at	R28636	2809	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	3.06	up	0.03678
rc_R31607_at	R31607	2813	EST	3.41	up	0.00163
rc_R33498_s_at	R33498	2820	EST	3.5	up	0.03336
rc_R39191_s_at	R39191	2834	KIAA1020 protein	5.18	up	0.03185
rc_R39390_at	R39390	2837	EST	4.18	up	0.0004
rc_R39610_s_at	R39610	2838	calpain, large polypeptide L2	3.13	up	0.01863
rc_R43952_at	R43952	2853	homeo box B5	3.39	up	0.04829
rc_R44617_f_at	R44617	2857	MyoD family inhibitor	6.54	up	0.02505
rc_R44793_at	R44793	2859	EST	5.4	up	0.00329
rc_R44839_at	R44839	2861	I-beta-1,3-N-acetylglucosaminyltransferase	5	up	0.01812
rc_R45569_at	R45569	2864	DKFZP547E1010 protein	3.96	up	0.00259
rc_R45994_f_at	R45994	2867	EST	6.48	up	0.00358
rc_R46079_f_at	R46079	2868	EST	3.03	up	0.00755
rc_R46337_s_at	R46337	2869	secretory carrier membrane protein 3	3.01	up	0.00374
rc_R48447_at	R48447	2871	EST	4.76	up	0.00533
rc_R48473_f_at	R48473	2872	EST	3.46	up	0.01196
rc_R48594_s_at	R48594	2875	EST	6.15	up	0.03831
rc_R49395_s_at	R49395	2881	EST	3.31	up	0.00867
rc_R49476_at	R49476	2883	EST	4.93	up	0.00763
rc_R49482_at	R49482	2884	EST	3.27	up	0.0161
rc_R49708_s_at	R49708	2886	EST	4.56	up	0.03767
rc_R51908_s_at	R51908	2892	EST	3.16	up	0.00083
rc_R52161_at	R52161	2893	EST	3.41	up	0.00053
rc_R52649_at	R52649	2894	EST	4.69	up	0.00135
rc_R53109_f_at	R53109	2899	dimethylarginine dimethylaminohydrolase 2	3.31	up	0.02406
rc_R54614_s_at	R54614	2902	EST	3.22	up	0.00334

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_R56095_s_at	R56095	2906	EST	3.67	up	0.0158
rc_R60512_s_at	R60512	2918	KIAA0191 protein	3.08	up	0.00856
rc_R61374_at	R61374	2921	EST	4.33	up	0.01489
rc_R61557_at	R61557	2922	KIAA0100 gene product	3.9	up	0.00292
rc_R62456_at	R62456	2925	EST	3.44	up	0.00285
rc_R66469_f_at	R66469	2937	pleckstrin and Sec7 domain protein	3.52	up	0.0272
rc_R70005_at	R70005	2944	EST	4.98	up	0.00007
rc_R70253_at	R70253	2945	EST	3.38	up	0.03125
rc_R70532_at	R70532	2947	EST	3.44	up	0.02186
rc_R70801_s_at	R70801	2950	EST	6.06	up	0.00291
rc_R71395_at	R71395	2952	EST	4.12	up	0.03719
rc_R72886_s_at	R72886	2956	KIAA0422 protein	5.5	up	0.00091
rc_R73569_s_at	R73569	2960	EST	3.54	up	0.01962
O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)						
rc_R76782_s_at	R76782	2963		3.73	up	0.00094
rc_R77451_l_at	R77451	2964	EST	3.67	up	0.00078
rc_R79246_f_at	R79246	2969	melanoma adhesion molecule	6.06	up	0.00057
rc_R91753_at	R91753	2983	EST	3.45	up	0.02391
rc_R91819_at	R91819	2984	EST	12.81	up	0.00037
rc_R92449_s_at	R92449	2985	KIAA0323 protein	4.34	up	0.00104
rc_R96527_s_at	R96527	2999	KIAA0253 protein	4.62	up	0.00702
rc_R96924_s_at	R96924	3001	EST	7.04	up	0.00012
S67070_at	S67070	3023	heat shock 27kD protein 2	3.12	up	0.01688
S78187_at	S78187	3036	cell division cycle 25B	4.83	up	0.00547
rc_T03438_s_at	T03438	3043	EST	3.79	up	0.02042
rc_T03580_f_at	T03580	3046	pyruvate kinase, muscle	5.57	up	0.01344
rc_T03749_at	T03749	3048	KIAA1089 protein	4.23	up	0.00776
rc_T10316_s_at	T10316	3052	EST	3.2	up	0.04794
rc_T10698_s_at	T10698	3054	EST	3.86	up	0.00195
rc_T15852_f_at	T15852	3062	EST	5.21	up	0.00642

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_T16206_s_at	T16206	3065	EST	4.29	up	0.00868
rc_T16226_at	T16226	3066	EST	7.23	up	0.00119
rc_T16550_at	T16550	3072	vacuolar protein sorting 45B (yeast homolog)	5.88	up	0.00004
rc_T16652_s_at	T16652	3073	BCS1 (yeast homolog)-like	3.63	up	0.00434
rc_T16983_s_at	T16983	3074	cleavage and polyadenylation specific factor 4, 30kD	4.23	up	0.0106
rc_T17066_s_at	T17066	3075	SET domain, bifurcated, 1	5.14	up	0.00073
rc_T17339_f_at	T17339	3076	EST	3.29	up	0.00669
rc_T17353_s_at	T17353	3077	EST	3.52	up	0.02085
rc_T23426_s_at	T23426	3079	EST	3.51	up	0.00674
rc_T23465_at	T23465	3081	EST	3.64	up	0.00265
rc_T23516_f_at	T23516	3083	3-phosphoglycerate dehydrogenase	3.39	up	0.00551
rc_T24068_s_at	T24068	3088	EST	8.65	up	0.00118
rc_T26471_at	T26471	3094	EST	3.76	up	0.0165
X-ray repair complementing defective repair in Chinese hamster cells 1						
rc_T26646_f_at	T26646	3097	X-ray repair complementing defective repair in Chinese hamster cells 1	3.49	up	0.02482
rc_T30214_at	T30214	3099	EST	4.46	up	0.03654
rc_T33489_s_at	T33489	3105	EST	4.6	up	0.00285
rc_T33508_s_at	T33508	3106	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	4.96	up	0.00064
rc_T33619_s_at	T33619	3107	EST	3.36	up	0.01283
rc_T33625_at	T33625	3108	EST	3.36	up	0.04096
rc_T33859_at	T33859	3109	KIAA0365 gene product	3.9	up	0.0019
potassium voltage-gated channel, shaker-related subfamily, beta member 2						
T34377_at	T34377	3111	potassium voltage-gated channel, shaker-related subfamily, beta member 2	4.55	up	0.00041
rc_T40439_s_at	T40439	3115	small nuclear ribonucleoprotein polypeptide B"	3.06	up	0.02842
rc_T41078_at	T41078	3121	bromodomain adjacent to zinc finger domain, 2B	3.08	up	0.03426
rc_T47032_s_at	T47032	3124	partner of RAC1 (arfaptin 2)	6.09	up	0.00019
rc_T47325_s_at	T47325	3125	EST	5.6	up	0.02923
ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)						
rc_T47969_s_at	T47969	3128	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	3.19	up	0.02283
rc_T51972_at	T51972	3140	EST	3.44	up	0.00406

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_T53590_s_at	T53590	3144	cytochrome P450, subfamily XIa (cholesterol side chain cleavage)	5.09	up	0.000002
rc_T55196_at	T55196	3147	EST	4.24	up	0.000046
rc_T58607_at	T58607	3155	EST	6.83	up	0.03711
rc_T59668_s_at	T59668	3160	lysyl oxidase	3.5	up	0.000083
rc_T62521_at	T62521	3168	EST	4.1	up	0.00392
rc_T62918_at	T62918	3169	EST	5.25	up	0.00687
rc_T65957_f_at	T65957	3176	ribosomal protein S3A	3.94	up	0.04187
rc_T66935_at	T66935	3179	EST	3.01	up	0.00123
rc_T67053_f_at	T67053	3180	EST	5	up	0.01846
rc_T77733_s_at	T77733	3219	tubulin, gamma 1	4	up	0.00526
rc_T78922_s_at	T78922	3222	stem cell growth factor; lymphocyte secreted C-type	3.89	up	0.00604
rc_T79477_s_at	T79477	3223	death-associated protein 6	4.4	up	0.00074
rc_T81393_s_at	T81393	3228	HMT1 (hnRNP methyltransferase, <i>S. cerevisiae</i>)-like 1	3.32	up	0.0023
rc_T88814_at	T88814	3242	EST	4.87	up	0.00001
rc_T89703_at	T89703	3244	EST	5.27	up	0.00019
rc_T90190_s_at	T90190	3247	H1 histone family, member 2	4.88	up	0.00555
rc_T94452_at	T94452	3257	EST	3.23	up	0.02245
rc_T95057_f_at	T95057	3259	EST	6.46	up	0.00613
rc_T97679_at	T97679	3266	EST	3.32	up	0.01566
rc_T99312_at	T99312	3270	EST	3.22	up	0.00084
U18018_at	U18018	3317	ets variant gene 4 (E1A enhancer-binding protein, E1AF)	3.9	up	0.0403
U18321_at	U18321	3318	death associated protein 3	3.14	up	0.00833
U24704_at	U24704	3332	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	3.45	up	0.00037
U26727_at	U26727	3337	cyclin-dependent kinase inhibitor 2A (melanoma, p16, Inhibits CDK4)	3.53	up	0.02913
U30825_at	U30825	3343	splicing factor, arginine/serine-rich 9	3.07	up	0.01928
U45285_at	U45285	3364	T-cell, immune regulator 1	5.75	up	0.00006
U47025_s_at	U47025	3368	phosphorylase, glycogen; brain	4.47	up	0.00037

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
U51586_at	U51586	3386	slah binding protein 1;FBP interacting repressor; Ro pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1	3.65	up	0.00403
U55206_at	U55206	3392	gamma-glutamyl hydrolase (conjugase, poly[polygamma-glutamyl hydrolase])	3.34	up	0.00315
U59321_at	U59321	3398	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17	3.12	up	0.02469
U62392_at	U62392	3403	zinc finger protein 193	3.56	up	0.0407
U66661_at	U66661	3406	gamma-aminobutyric acid (GABA) A receptor, epsilon	3.55	up	0.0045
U68142_at	U68142	3411	RAB2, member RAS oncogene family-like SHC (Src homology 2 domain-containing) transforming protein 1	3.02	up	0.0296
U73377_at	U73377	3417	ubiquitin carrier protein E2-C	4.64	up	0.00081
U73379_at	U73379	3418	apoptosis inhibitor 4 (survivin)	3.32	up	0.00808
U75285_mna1_at	U75285	3422	ribonuclease 6 precursor	5.32	up	0.01127
U85625_at	U85625	3448	nuclear RNA helicase, DECD variant of DEAD box family	4	up	0.01664
U90426_at	U90426	3453	H2A histone family, member L	3.24	up	0.00035
U90551_at	U90551	3457	EST	3.54	up	0.01523
U90904_at	U90904	3458	adaptor-related protein complex 3, delta 1 subunit	3.02	up	0.00381
U91930_at	U91930	3460	EST	3.68	up	0.00009
rc_W02041_at	W02041	3466	EST	5.34	up	0.00027
rc_W02695_at	W02695	3467	EST	3.1	up	0.04745
rc_W04507_s_at	W04507	3469	prefoldin 4	3.02	up	0.04091
rc_W04550_at	W04550	3470	EST	4.01	up	0.00349
rc_W15495_at	W15495	3474	chromosome 21 open reading frame 5	3.09	up	0.00491
W26716_at	W26716	3482	non-histone chromosome protein 2 (<i>S. cerevisiae</i>)-like 1	5.47	up	0.00146
W28362_at	W28362	3488	KIAA0974 protein	4.38	up	0.00322
W28366_at	W28366	3489	EST	3.21	up	0.01007
rc_W31906_at	W31906	3497	secretagogin	6.62	up	0.00926
rc_W42627_f_at	W42627	3511	EST	4.37	up	0.00021
rc_W42674_at	W42674	3512	EST	3.07	up	0.0261
rc_W42778_at	W42778	3513	EST	3.27	up	0.02411
rc_W42788_at	W42788	3514	deoxynucleotidyltransferase, terminal	3.24	up	0.02261

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_W42957_at	W42957	3516	calmodulin 2 (phosphorylase kinase, delta)	5.79	up	0.03689
rc_W44557_at	W44557	3518	chromosome 1 open reading frame 2	4.1	up	0.00433
rc_W45320_f_at	W45320	3523	KRAB-associated protein 1	10.05	up	0.00002
rc_W46286_s_at	W46286	3526	EST	3.68	up	0.00311
rc_W46634_at	W46634	3530	EST	5.03	up	0.02152
rc_W46810_s_at	W46810	3531	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2	3.17	up	0.03434
rc_W46846_at	W46846	3532	EST	5.11	up	0.00025
rc_W46947_at	W46947	3533	EST	3.42	up	0.04665
rc_W47206_at	W47206	3535	EST	3.23	up	0.01931
W49743_at	W49743	3540	EST	3.11	up	0.01121
rc_W49791_at	W49791	3541	plasminogen activator, tissue	3.58	up	0.02438
rc_W56642_at	W56642	3547	EST	3.15	up	0.00654
rc_W57931_at	W57931	3549	EST	3.01	up	0.02661
rc_W58081_at	W58081	3550	neuroendocrine-specific protein C like (foocen)	3.05	up	0.03767
W58247_s_at	W58247	3551	kinesin family member 4	3.08	up	0.00048
rc_W60097_at	W60097	3556	DEAD/H (Asp-Glu-Ala-Asp)/His box polypeptide, Y chromosome	4.82	up	0.04903
rc_W60486_at	W60486	3558	EST	4.27	up	0.00446
rc_W63608_at	W63608	3564	EST	3.33	up	0.02443
W69302_at	W69302	3573	EST	4.37	up	0.00165
rc_W69468_at	W69468	3574	EST	3.25	up	0.00055
rc_W70336_at	W70336	3579	EST	4.46	up	0.00023
rc_W72187_at	W72187	3582	EST	3.09	up	0.00134
rc_W72276_at	W72276	3583	EST	3.56	up	0.0476
rc_W73038_at	W73038	3588	EST	4.83	up	0.00902
rc_W74536_s_at	W74536	3598	advanced glycosylation end product-specific receptor	3.07	up	0.00251
rc_W778057_at	W778057	3600	EST	5.53	up	0.01231
rc_W79421_at	W79421	3603	EST	3.57	up	0.00895
rc_W79773_at	W79773	3605	EST	4.89	up	0.00034
rc_W80730_at	W80730	3607	EST	3.35	up	0.01526
rc_W80763_at	W80763	3608	EST	4.98	up	0.01026

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_W80852_at	W80852	3609	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	6.37	up	0.00005
rc_W81654_at	W81654	3616	SRY (sex determining region Y)-box 13	6.06	up	0.00127
rc_W84447_at	W84447	3617	EST	3.34	up	0.00986
rc_W85875_at	W85875	3620	EST	4.91	up	0.01198
rc_W86214_at	W86214	3625	EST	4.3	up	0.00194
rc_W86748_at	W86748	3629	EST	5.09	up	0.01882
rc_W90146_f_at	W90146	3644	EST	3.58	up	0.00322
rc_W92608_s_at	W92608	3653	BAL1-associated protein 3	4.84	up	0.00599
rc_W94281_s_at	W94281	3658	integral membrane protein 2C	3.51	up	0.01689
rc_W94885_at	W94885	3660	EST	6.53	up	0
rc_W95841_at	W95841	3666	EST	3	up	0.00466
X04347_s_at	X04347	3680	heterogeneous nuclear ribonucleoprotein A1	3.34	up	0.00123
X05610_at	X05610	3685	collagen, type IV, alpha 2	6.04	up	0.00062
X06700_s_at	X06700	3688	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	3.58	up	0.02964
X14487_mn1_s_at	X14487	3702	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	3.19	up	0.01268
X14850_at	X14850	3706	H2A histone family, member X	3.13	up	0.01523
X17567_s_at	X17567	3719	small nuclear ribonucleoprotein polypeptides B and B1	3.96	up	0.00317
X53331_at	X53331	3727	matrix Gla protein	3.95	up	0.0151
X54667_s_at	X54667	3731	cystatin S, cystatin SN	3.51	up	0.00187
X54941_at	X54941	3732	CDC28 protein kinase 1	3.99	up	0.0016
X54942_at	X54942	3733	CDC28 protein kinase 2	3.8	up	0.0035
X56494_at	X56494	3738	pyruvate kinase, muscle	3.65	up	0.04795
X57129_at	X57129	3743	H1 histone family, member 2	4.63	up	0.00663
X57809_s_at	X57809	3746	immunoglobulin lambda locus	3.64	up	0.02655
X62153_s_at	X62153	3754	minichromosome maintenance deficient (<i>S. cerevisiae</i>) 3	3.44	up	0.00704
X62534_s_at	X62534	3755	high-mobility group (nonhistone chromosomal) protein 2	3.39	up	0.0186
X64364_at	X64364	3764	basigin	3.57	up	0.00902
X66899_at	X66899	3772	Ewing sarcoma breakpoint region 1	3.41	up	0.03777

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	P value
X69910_at	X69910	3787	transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment	3.35	up	0.00898
X74801_at	X74801	3791	chaperonin containing TCP1, subunit 3 (gamma)	3.86	up	0.00453
X79536_at	X79536	3804	heterogeneous nuclear ribonucleoprotein A1	3.06	up	0.00449
X83425_at	X83425	3812	Lutheran blood group (Auberger b antigen included)	3.66	up	0.02661
X87212_at	X87212	3816	cathepsin C	3.45	up	0.02486
X92896_at	X92896	3829	DNA segment on chromosome X (unique) 9879 expressed sequence	3.1	up	0.0405
X99920_at	X99920	3843	S100 calcium-binding protein A13	4.66	up	0.00113
Y00705_at	Y00705	3850	serine protease inhibitor, Kazal type 1	28.88	up	0.00003
Y00764_at	Y00764	3851	ubiquinol-cytochrome c reductase hinge protein	3.04	up	0.01294
Y08302_at	Y08302	3852	dual specificity phosphatase 9	3.48	up	0.00787
Y08999_at	Y08999	3855	actin related protein 2/3 complex, subunit 1A (41 kD) eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	3.13	up	0.02376
Z21507_at	Z21507	3867	heat shock 27kD protein 1	3.57	up	0.01898
Z23090_at	Z23090	3868	nucleotide exchange protein	3.69	up	0.00628
Z24727_at	Z24727	3871	tropomyosin 1 (alpha)	3.64	up	0.00388
Z37987_s_at	Z37987	3882	glypican 3	10.66	up	0.02304
rc_Z38299_at	Z38299	3887	EST	3.71	up	0.0036
rc_Z38431_at	Z38431	3889	EST	3.09	up	0.0083
rc_Z38444_at	Z38444	3891	KIAA0923 protein	3.38	up	0.02918
rc_Z38462_at	Z38462	3892	KIAA0938 protein	4.69	up	0.0142
rc_Z38904_at	Z38904	3896	EST	3.02	up	0.00814
rc_Z39191_at	Z39191	3901	EST	3.47	up	0.00756
rc_Z39200_at	Z39200	3902	EST	4.07	up	0.00075
rc_Z39379_at	Z39379	3903	EST	3.77	up	0.00513
rc_Z39429_at	Z39429	3906	EST	3.58	up	0.00416
rc_Z39682_s_at	Z39682	3911	KIAA0954 protein	6.96	up	0.01966
rc_Z40006_at	Z40006	3917	EST	3.54	up	0.00156
rc_Z40883_r_at	Z40883	3924	EST	3.26	up	0.01863
rc_Z41349_at	Z41349	3931	EST	3.45	up	0.01503

Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	Fold Change	Direction	Pvalue
rc_Z41747_at	Z41747	3936	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	3.04	up	0.01336
Z47727_at	Z47727	3940	polymerase (RNA) II (DNA directed) polypeptide K	3.28	up	0.00317
Z74615_at	Z74615	3949	collagen, type I, alpha 1	5.47	up	0.00283
Z74616_s_at	Z74616	3950	collagen, type I, alpha 2	5.95	up	0.02212

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	DEK oncogene (DNA binding)	fold change in hcc		hcc sample set 2:		hcc sample set 2:		hcc sample set 2:		normal set 2: median		normal set 2: std dev	
				set 2	p value	Mean	Median	Std Dev	Mean	Median	Std Dev				
AA093497_s_at	AA093497	199	#N/A	180.58	107.64	165.71	52.11	48.84	18.96	21.63	21.63	45.59	102.24	26.51	
AA248283_s_at	AA248283	534	EST	#N/A	67.18	45.86	55.18	11.71	629.13	#N/A	#N/A	63.36	20.23	11.71	
AA291456_s_at	AA291456	700	EST	#N/A	828.34	830.24	196.63	629.13	509.58	671.21	671.21	14.7	20.64	4.33	
AA400643_s_at	AA400643	817	GAS2-related on chromosome 22	4.04	0.03751	118.72	123.18	137.15	-43.6	-33.96	-33.96	60.39			
AA421079_at	AA421079	930	EST	#N/A	#N/A	37.17	34.26	18.5	15.27	16.75	16.75	15.28			
AA428172_f_at	AA428172	986	Notch (Drosophila) homolog	9.63	0.00195	335.57	374.9	231.52	-9.64	-15.61	-15.61	56.16			
AA464043_s_at	AA464043	1255	EST	3.99	0.00056	116.97	115.99	53.49	14.27	10.06	10.06	25.86			
H19562_at	H19562	1896	PTD010 protein	#N/A	#N/A	522.13	432.85	256.94	393.61	326.53	326.53	182.71			
L08044_s_at	L08044	2149	tretolipase factor 3 (intestinal)	#N/A	#N/A	214.6	108.17	238.79	107.82	58.55	58.55	184.16			
L29218_s_at	L29218	2190	CDC-like kinase 2	6.51	0.00019	219.64	237.35	104.29	6.53	-10.03	-10.03	59.8			
L37747_s_at	L37747	2206	lamin B1	#N/A	#N/A	43.42	28.65	37.33	5.97	5.1	5.1	7.57			
N34257_at	N34257	2495	EST	#N/A	#N/A	20.76	21.48	19.54	-1.84	-2.74	-2.74	8.53			
R50692_at	R50692	2888	KIAA0476 gene product	#N/A	#N/A	197.89	187.87	101.08	148.53	151.12	151.12	63.03			
R60368_at	R60368	2917	EST	#N/A	#N/A	29.68	28.93	31.9	-28.29	-26.44	-26.44	41.68			
R66475_at	R66475	2938	EST	#N/A	#N/A	45.68	32.34	34.37	7.64	8.26	8.26	6.3			
T34377_at	T34377	3111	potassium voltage-gated channel, shaker-related subfamily, beta member 2	4.55	0.00041	113.59	120.58	51.65	6.87	11.17	11.17	25.69			
U75968_s_at	U75968	3423	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase)	#N/A	#N/A	187.33	200.16	90.35	115.5	102.24	102.24	77.72			
W21426_at	W21426	3481	KIAA0806 gene product	#N/A	#N/A	63.36	64.93	20.23	45.59	40.39	40.39	19.89			
W28696_i_at	W28696	3491	EST	#N/A	#N/A	14.7	20.64	17.12	4.28	4.33	4.33	2.47			

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change		hcc		hcc		hcc		normal		normal	
				In hcc	set 2:	sample	set 2:	sample	set 2:	sample	set 2:	Mean	Median	Std Dev	set 2:
X57129_at	X57129	3743	H1 histone family, member	4.63	0.00663	137.13	137.75	87.31	8.38	5.39	5.39	28.3	28.3	28.3	28.3
rc_AA024658_at	AA024658	47	ribosomal protein S19	7.55	0.00592	278.11	120.83	373.3	7.62	5.03	5.03	10.68	10.68	10.68	10.68
rc_AA029288_at	AA029288	65	EST	3.36	0.04908	134.53	56.15	209.69	4.09	3.35	3.35	8.39	8.39	8.39	8.39
rc_AA037828_at	AA037828	88	KIAA0614 protein	#N/A	#N/A	53.61	46.86	41.68	13.32	1.65	1.65	11.96	11.96	11.96	11.96
rc_AA040465_at	AA040465	95	EST	3.63	0.01806	229.8	210.67	180.94	47.15	45.53	45.53	5.48	5.48	5.48	5.48
rc_AA053660_at	AA053660	128	EST	#N/A	#N/A	543.66	223.47	685.44	95.24	79.97	79.97	42.99	42.99	42.99	42.99
rc_AA136332_at	AA136332	299	cAMP responsive element binding protein 3 (luman)	#N/A	#N/A	49.04	33.07	31.07	-18.27	-20.23	-20.23	13.05	13.05	13.05	13.05
rc_AA149530_at	AA149530	324	interferon regulatory factor 3	#N/A	#N/A	32.94	23.12	34.23	4.21	5.38	5.38	8.53	8.53	8.53	8.53
rc_AA149586_at	AA149586	325	EST	#N/A	#N/A	24.99	26.6	34.37	5.26	9.11	9.11	23.41	23.41	23.41	23.41
rc_AA206023_at	AA206023	427	EST	#N/A	#N/A	154.13	170.36	85.33	108.57	111.76	111.76	58.39	58.39	58.39	58.39
rc_aa234530_s_at	AA234530	484	N-ethylmaleimide-sensitive factor	#N/A	#N/A	143.67	135.48	82.59	51.33	42.9	42.9	35.02	35.02	35.02	35.02
rc_AA251909_at	AA251909	549	EST	3.59	0.01129	92.19	79.34	72.73	8.88	11.22	11.22	8.27	8.27	8.27	8.27
rc_AA262030_at	AA262030	605	EST	#N/A	#N/A	119.75	89.66	103.84	31.51	32.91	32.91	14.46	14.46	14.46	14.46
rc_AA262477_at	AA262477	608	ribonuclease HI, large subunit	4.57	0.00724	242.42	199.5	182.26	44.51	36.87	36.87	22.37	22.37	22.37	22.37
rc_AA283759_at	AA283759	671	EST	#N/A	#N/A	91.82	76.73	42.28	46.87	45.86	45.86	21.54	21.54	21.54	21.54
rc_AA291644_at	AA291644	701	EST	3.28	0.00033	114.73	117.29	44.59	32.77	30.24	30.24	21.1	21.1	21.1	21.1
rc_AA338760_at	AA338760	744	EST	3.96	0.01307	129.77	130.26	87.27	14.91	21.91	21.91	26.96	26.96	26.96	26.96
rc_AA398205_at	AA398205	789	EST	4.22	0.00059	125.4	107.84	63.85	15.01	7.37	7.37	26.26	26.26	26.26	26.26
rc_AA401965_at	AA401965	833	tumor suppressor deleted in oral cancer-related 1	7.58	0.00089	932.74	924.02	593.69	120.58	93.29	93.29	109.41	109.41	109.41	109.41
rc_AA402272_at	AA402272	837	EST	3.73	0.02336	348.91	340	230.15	99.7	92.28	92.28	80.27	80.27	80.27	80.27
rc_AA404597_at	AA404597	854	EST	#N/A	#N/A	609.98	525.02	371.31	379.26	336.33	336.33	167.43	167.43	167.43	167.43
rc_AA417030_at	AA417030	914	EST	7.35	0.00555	200.3	168.21	135.63	6.42	7.5	7.5	7.77	7.77	7.77	7.77

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			hcc			hcc		
			In hcc	set 2	p value	sample set:	sample set 2:	sample set 2:	normal set 2:	normal set 2:	Median set 2:
rc_AA423820_at	AA423820	940 EST	#N/A	#N/A	111.38	111.23	120.84	41.9	21.93	44.58	
rc_AA425852_1_at	AA425852	958 EST	3.82	0.0395	131.52	95.35	166.76	7.02	5.22	4.75	
rc_AA430032_at	AA430032	1009 1 pituitary tumor-transforming	10.67	0.00052	377.69	320.44	294.49	26.8	15.31	35.24	
rc_AA430673_at	AA430673	1017 EST	#N/A	#N/A	45.74	34.15	44.8	-1.21	3.63	15.26	
rc_AA443321_at	AA443321	1076 EST	#N/A	#N/A	33.93	32.89	11.76	10.79	9.65	7.26	
rc_AA443941_at	AA443941	1085 tumor suppressing	#N/A	#N/A	97.74	103.38	47.48	31.09	34.9	16.61	
rc_AA447223_at	AA447223	1100 EST	#N/A	#N/A	31.66	18.91	31.1	4.45	3.74	6.5	
rc_aa449431_s_at	AA449431	1124 IF2	3.76	0.00571	94.41	95.64	54.08	17.4	16.86	5.38	
rc_AA454597_s_at	AA454597	1166 EST	4.23	0.00917	342.59	311.81	207.71	66.6	57.29	23.41	
rc_AA458882_at	AA458882	1205 EST	#N/A	#N/A	93.56	52.28	98.72	24.97	22.52	17.66	
rc_AA458934_at	AA458934	1208 EST	#N/A	#N/A	33.6	28.19	29.02	7.1	7.91	4.22	
rc_AA465342_at	AA465342	1271 EST	3.21	0.01378	131.07	109.99	95.4	30.07	33.06	23.97	
rc_AA477561_at	AA477561	1292 EST	#N/A	#N/A	146.3	127.03	97.99	63.83	76.56	37.87	
rc_AA491295_at	AA491295	1390 calcium/calmodulin-dependent protein kinase kinase 2, beta	3.71	0.0103	180.61	173.47	118.85	46.95	31.51	65.56	
rc_AA608545_at	AA608545	1462 RAD51 (S. cerevisiae) homolog (E. coli RecA homolog)	#N/A	#N/A	70.5	57.51	53.36	7.76	8.92	6.17	
rc_AA620553_s_at	AA620553	1504 flap structure-specific endonuclease 1	7.56	0.00101	262.87	232.63	201.66	14.44	4.85	38.53	
rc_AA621325_at	AA621325	1522 HNK-1 sulfotransferase	#N/A	#N/A	74.57	70.64	46.61	27.23	25.89	16.03	
rc_AA621780_at	AA621780	1530 CGI-96 protein	#N/A	#N/A	81.72	92.23	49.69	12.06	11.27	19.2	
rc_F02807_at	F02807	1781 KIAA0838 protein	5.67	0.02064	260.02	219.01	229.96	20.93	16.66	22.24	

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in hcc		hcc		hcc		hcc		hcc	
			set 1	p value	sample set 2:	Mean	Median	Std Dev	sample set 2:	Mean	Median	Std Dev
rc_F04444_at	F04444	1788 EST	4.13	0.00944	371.21	360.5	186.45	119.68	121.27	109.82		
rc_F04524_s_at	F04524	1790 stomatin-like protein 1	#N/A	#N/A	117.77	135.65	68.29	46.56	44.53	33.75		
rc_F08876_at	F08876	1797 EST	9.06	0	209.64	201.85	53.21	-22.5	-20.17	37.21		
rc_F10161_at	F10161	1811 EST	#N/A	#N/A	50.78	46.73	32.42	15.4	14.78	11.87		
rc_F10453_at	F10453	1819 EST	3.64	0.01878	135.07	138.53	85.7	27.28	14.2	54.04		
rc_H04649_at	H04649	1838 EST	#N/A	#N/A	180.25	158.18	164.34	50.86	41.2	33.9		
rc_H04793_at	H04793	1840 DKFZP434F091 protein	#N/A	#N/A	23.18	20	41.25	-14.45	-20.45	29		
rc_H59617_at	H59617	1964 EST	5.81	0.0115	212.68	209.19	157.42	19.24	21.65	16.88		
rc_H97012_at	H97012	2058 EST	3.51	0.03505	171.34	138.12	170.68	27.69	38.46	36.08		
rc_H98657_at	H98657	2068 EST	#N/A	#N/A	141.17	131.42	69.63	111.2	84.74	128.92		
rc_N23319_at	N23319	2454 EST	#N/A	#N/A	70.62	66.39	49.4	13.74	8.56	21.62		
rc_N23868_at	N23868	2459 EST	#N/A	#N/A	79.69	81.67	56.06	20.52	20.19	11.48		
rc_N45224_at	N45224	2516 EST	#N/A	#N/A	349.73	360.67	164.87	215.49	223.16	151.06		
rc_N48595_at	N48595	2528 EST	#N/A	#N/A	85.77	67.62	51.78	28.84	29.38	8.3		
rc_N75541_at	N75541	2692 EST	4.43	0.01059	182.83	131.35	183.41	34.1	15.82	56.07		
ras homolog gene family, member H												
rc_N90273_s_at	N90273	2713	#N/A	#N/A	105.53	96.01	41.89	68.92	59.56	35.69		
rc_n93465_s_at	N93465	2735 EST	#N/A	#N/A	803.68	716.56	385.5	624.57	694.14	306.11		
rc_R39191_s_at	R39191	2834 KIAA1020 protein	5.18	0.03185	331.72	80.62	590.96	17.46	18.33	16.04		
rc_R44793_at	R44793	2859 EST	5.4	0.00329	155.86	121.83	125.26	10.1	7.86	16.54		
rc_R44817_at	R44817	2860 EST	#N/A	#N/A	594.46	602.82	206.15	255.91	249.29	69.09		
rc_R44896_at	R44896	2862 KIAA0665 gene product	#N/A	#N/A	67.08	57.13	34.18	19.1	20.75	23.04		
rc_R64137_s_at	R64137	2931 EST	#N/A	#N/A	31.25	24.23	21	2.9	2.65	6.94		
rc_R71395_at	R71395	2952 EST	4.12	0.03719	166.03	99.42	190.98	14.99	12.28	14.58		
rc_R72087_at	R72087	2955 EST	#N/A	#N/A	262.11	302.11	95	201.97	183.76	83.41		
rc_R91819_at	R91819	2984 EST	12.81	0.00037	467.79	364.2	426.16	11.34	9.35	36.49		
rc_T03749_at	T03749	3048 KIAA1089 protein	4.23	0.00776	103	97.55	74.34	-5.18	-6.08	13.69		
rc_T25744_s_at	T25744	3092 EST	#N/A	#N/A	72.74	73.3	37.84	15.56	13.18	12.65		

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change in hcc set 2:	hcc		hcc		normal set 2: Median		normal set 2: Median	
					p value	Mean	sample set 2: Median	Std Dev	Mean	Std Dev	Mean	Std Dev
rc_T62918_at	T62918	3169	EST	5.25	0.00687	136.22	142.37	83.63	-12.41	-6.89	17.59	
rc_T89731_at	189731	3245	EST	#N/A	#N/A	63.59	65.07	20.47	5.75	3.83	11.8	
rc_W32176_s_at	W32176	3498	STE24 (yeast, homolog) zinc metalloprotease, rab6 GTPase activating protein (GAP and centrosome-associated)	#N/A	#N/A	550.53	614.92	234.79	290.18	277.95	129.45	
rc_W47388_at	W47388	3536	EST	#N/A	#N/A	97.33	71	59.73	43.93	36.52	48.34	
rc_W78057_at	W78057	3600	EST	5.53	0.01231	265.23	222.35	199.24	29.21	29.9	34.33	
rc_W80763_at	W80763	3608	EST	4.98	0.01026	147.37	138.37	122.38	16.84	15.48	9.22	
rc_W90146_f_at	W90146	3644	EST	3.58	0.00322	82.11	69.02	47.2	9.93	8.63	6.49	
rc_Z38299_at	Z38299	3887	EST	3.71	0.0036	140.86	127.16	96.62	30.48	25.94	23.34	
rc_Z38404_at	Z38404	3888	EST	#N/A	#N/A	59.77	56.71	37.29	29.82	30.16	9	
rc_Z38462_at	Z38462	3892	KIAA0938 protein	4.69	0.0142	137.19	116.11	116.16	-0.86	0.53	7.64	
rc_Z38688_at	Z38688	3893	EST	#N/A	#N/A	49.85	46.83	42.25	21.38	13.4	29.47	
rc_Z38729_at	Z38729	3894	EST	#N/A	#N/A	77.67	57.81	60.7	-2.4	-5.01	46.96	
rc_Z40556_at	Z40556	3921	CGI-96 protein	#N/A	#N/A	176.19	76.96	285.02	59.62	55.07	16.66	
rc_AA021549_at	AA021549	42	EST	3.17	0.00158	100.01	83.02	44.39	31.74	20.12	36.74	
rc_AA026270_at	AA026270	56	tyrosyl-tRNA synthetase	#N/A	#N/A	269.96	261.31	191.51	76.85	76.68	45.22	
rc_AA055896_at	AA055896	135	collagen, type V, alpha 1	10.87	0.00907	414.16	454.82	330.75	-3.14	-5.8	33.88	
rc_AA112979_s_at	AA112979	225	vaccinia related kinase 1	#N/A	#N/A	37.93	31.05	16.86	8.54	8.02	2.59	
rc_AA134063_at	AA134063	286	EST	#N/A	#N/A	25.71	13.84	34.35	-5.21	-6.17	6	
rc_AA150053_at	AA150053	327	EST	#N/A	#N/A	270.14	248.87	144.92	101.87	88.37	73.73	
rc_AA206914_at	AA206914	428	EST	#N/A	#N/A	89.35	94.1	46.27	66.34	69.2	26.35	
rc_AA243133_at	AA243133	525	serine/threonine kinase 15	7.03	0.00005	147.5	162.28	43.03	9.69	12.1	9.8	
rc_AA243466_at	AA243466	527	EST	#N/A	#N/A	61.94	42.38	37.6	13.66	13.42	9.63	
rc_AA243598_at	AA243598	531	EST	#N/A	#N/A	60.15	62.79	32.67	11.41	13.18	13.43	
rc_AA252147_at	AA252147	551	EST	#N/A	#N/A	95.91	56.69	122.31	3.65	-0.82	22.5	
rc_AA255566_at	AA255566	570	EST	#N/A	#N/A	64.28	50.15	52.25	16.18	14.38	13.17	

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	fold change In hcc		hcc sample set 2:		hcc sample set 2:		hcc sample set 2:		normal set 2: set 2:		
			set 2:	p value	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median	
rc_AA279667_s_at	AA279667	629 EST	#N/A	184.99	102.43	289.71	8.06	7.61	23.78				
rc_AA279943_s_at	AA279943	635 EST	#N/A	137.05	63.54	232.2	-4.7	-5.33	11.18				
rc_AA290594_s_at	AA290594	691 EST	#N/A	59.19	56.31	23.84	21.4	18.8	23.98				
rc_AA290776_s_at	AA290776	693 EST	#N/A	524.07	516.6	88.67	441.83	355.04	245.84				
rc_AA292765_at	AA292765	712 ZW10 interactor	7.24	0.00498	202.52	192.15	142.78	11.33	18.29	13.27			
rc_AA398908_at	AA398908	801 EST	20.72	0.00114	629.56	433.87	551.97	-174.29	-216.08	104.42			
rc_AA405098_at	AA405098	855 EST	6.09	0.01224	221.56	130.95	237.73	-4.35	-8.44	30.78			
rc_AA406542_at	AA406542	878 EST	#N/A	179.08	84.98	218.93	-1.99	-1.49	12.75				
rc_AA435738_at	AA435738	1042 EST	#N/A	80.97	82	30.96	50.41	51.29	33.08				
rc_AA443585_at	AA443585	1077 EST	#N/A	200.3	136.72	140.42	118.18	97.38	102.71				
rc_AA446596_at	AA446596	1092 factor, mitochondrial	#N/A	103.35	97.42	153.31	72.58	70.64	154.24				
rc_AA447777_at	AA447777	1107 EST	#N/A	258.37	212.57	171.93	133.78	116.63	56.34				
rc_AA453757_at	AA453757	1156 EST	#N/A	128.41	118.8	40.54	65.66	70.33	40.45				
rc_AA459254_at	AA459254	1211 EST	6.22	0.00001	309.74	308.36	112.62	51.84	43.51	37.57			
rc_AA459673_at	AA459673	1220 polypeptide C	#N/A	32.11	31.27	15.41	8.91	6.74	8.86				
rc_AA476233_at	AA476233	1282 EST	#N/A	52.26	34.54	55.5	9.04	14.67	24.04				
rc_AA496993_at	AA496993	1405 EST	#N/A	91.01	73.62	80.93	24.83	12.83	29.07				
rc_AA504512_s_at	AA504512	1415 KIAA0943 protein	5.72	0.00384	316.32	322.55	180.22	65.48	28.37	93.94			
rc_AA609132_at	AA609132	1479 EST	#N/A	67.33	42.61	65.11	29.14	23.25	53.79				
rc_AA609942_at	AA609942	1494 EST	#N/A	89.98	66.8	71.4	15.89	14.41	25.58				
rc_F02254_s_at	F02254	1777 serine/threonine kinase	5.1	0.00329	376.8	341.06	145.28	90	72.97	135.39			
rc_H48459_s_at	H48459	1937 KIAA0186 gene product	3.1	0.02325	71.21	49.95	87.89	-29.4	-30.17	6.19			
rc_H87790_at	H87790	2018 EST	#N/A	284.91	287.54	145.66	466.07	547.34	192.71				
rc_N34017_at	N34017	2494 EST	#N/A	39.35	37.49	4.67	5.47	7.05	10.01				
rc_N35493_at	N35493	2502 EST	#N/A	73.6	80.62	31.24	19.03	18.75	17				

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in hcc		hcc sample		hcc sample		normal set 2:		normal set 2:		
			set 2	p value	Mean	Median	Std Dev	Mean	Median	Std Dev	set 2:	set 2:	
rc_N63604_at	N63604	2601	EST	#N/A	47.18	32.72	35	16.51	14.36	10.5			
rc_N63646_at	N63646	2602	EST	#N/A	479.9	367.24	240.56	182.22	137.95	90.9			
rc_N69014_s_at	N69014	2642	region Y-box 22	#N/A	193.21	174.83	48.23	116.34	129.47	50.74			
rc_N69879_s_at	N69879	2651	drebbrin 1	3.15	0.01659	88.78	84.86	61.76	3.69	-2.94	21.49		
rc_N69983_at	N69983	2652	EST	#N/A	93.25	96.86	49.82	76.2	93.14	54.92			
rc_N70330_at	N70330	2656	EST	#N/A	108.39	69.74	105.54	33.78	27.33	16.47			
rc_N74018_at	N74018	2684	EST	#N/A	22.65	25.34	10.26	2.34	1.47	10.41			
rc_N89670_at	N89670	2709	EST	#N/A	65.03	59.18	66.58	3.16	-1.81	43.32			
rc_N93000_at	N93000	2727	EST	#N/A	77.68	64.15	45.06	17.65	18.66	10.91			
rc_N99944_s_at	N99944	2749	EST	3.46	0.00104	211.02	200.61	102.49	60.05	50.12	29.73		
rc_R97176_at	R97176	3002	EST	#N/A	143.07	152.08	86.96	53.41	58.28	38.91			
rc_T16226_at	T16226	3066	EST	7.23	0.00119	323.53	312.1	209.59	33.87	22.78	38.68		
rc_T32108_at	T32108	3103	EST	#N/A	180.81	165.53	68.41	148.09	152.11	92.06			
rc_W15275_s_at	W15275	3472	EST	#N/A	33.62	31.78	35.23	30.09	24.85	43.25			
rc_W31906_at	W31906	3497	secretagogin	6.62	0.00926	474.89	174.52	605.68	42.41	30.95	47.65		
rc_W46286_s_at	W46286	3526	EST	3.68	0.00311	154.73	166.08	72.64	23.51	22.85	61.89		
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y			chromosome		4.82		0.04903		235.42		265.15		
KDEL (Lys-Asp-Glu-Leu)			endoplasmic reticulum		6.37		0.00005		184.61		159.98		
protein retention receptor 3			Wolf-Hirschhorn syndrome candidate 1		3.33		0.00648		73.04		72.71		
rc_W80852_at			AA046745		3.36		0.00088		100.81		106.86		
rc_AA046745_at			AA052941		121		EST		#N/A		44.56		
rc_AA052941_at			AA058589_f_at		144		EST		#N/A		44.63		
rc_AA058589_f_at			AA126561_s_at		249		stannocalcin		#N/A		51.44		
rc_AA126561_s_at			AA126561		31.6		7.16		31.6		7.73		

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in hcc		hcc sample set 2:		hcc sample set 2:		normal set 2:		normal set 2:		
			set 2: p value	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev	
rc_AA146849_s_at	AA146849	313 target of myb1 (chicken homolog)	4.72	0.00326	398.05	341.23	244.73	98.86	106.97	86.19			
rc_AA149889_at	AA149889	326 anchoring protein 95	8.55	0.00224	240.81	312.86	143.89	-0.24	8.25	29.83			
rc_AA283711_s_at	AA283711	669 ubiquitin carrier protein EST	#N/A	#N/A	382.91	380.33	210.95	221.7	203.51	93.54			
rc_AA284153_at	AA284153	673 #N/A	#N/A	#N/A	117.98	127.81	72.86	53.98	43.58	32.17			
rc_AA335191_f_at	AA335191	741 creatine kinase, brain TNF receptor-associated factor 1	6.47	0.01462	512.64	199.99	673.92	43.84	33.21	43.52			
rc_AA402642_s_at	AA402642	840 ATP-binding cassette, subfamily F (GCN20), member 2	#N/A	#N/A	137.67	59.13	211.07	35.93	19.15	31.32			
rc_AA427460_s_at	AA427460	972 v-Ha-ras Harvey rat sarcoma viral oncogene EST	#N/A	#N/A	190.92	187.57	78.83	92.5	83.63	49.3			
rc_AA431429_at	AA431429	1021 #N/A	#N/A	#N/A	25.39	21.98	9.32	5.32	4.23	4.43			
rc_AA443316_s_at	AA443316	1075 homolog	3.4	0.00133	138.89	124.06	70.22	40.07	41.12	32.54			
rc_AA476260_at	AA476260	1280 EST ubiquitin-conjugating enzyme E2L 3	#N/A	#N/A	61.23	69.49	40.45	-32.66	-15.85	56.91			
rc_AA487058_at	AA487058	1352 KIAA0530 protein	3.33	0.00211	113.43	106.74	60.79	28.44	29.54	18.61			
rc_AA521149_at	AA521149	1420 EST	#N/A	#N/A	53.83	48.84	25.7	7.71	6.06	7.11			
rc_AA599244_at	AA599244	1448 AA599850	3.55	0.03215	122.91	75.32	123.52	-1.23	-2.33	31.86			
rc_AA599850_at	AA599850	1457 AA621530	3.26	0.00298	78.73	75.43	40.45	12.46	15.12	13.43			
rc_AA621530_at	AA621530	1526 AA621644	#N/A	#N/A	83.13	88.29	43.19	71.19	66.84	29.87			
rc_AA621644_at	AA621644	1528 C15078_I_at	#N/A	#N/A	121.71	98.25	100.16	26.22	31.14	60.2			
rc_C15078_I_at	C15078	1573 D80710_f_at	3.17	0.04549	153.76	74.74	166.28	22.95	28.29	24.59			
rc_D80710_f_at	D80710	1734 integral type I protein	#N/A	#N/A	70.05	77.71	32.11	41.25	43.53	17.46			
rc_D80948_f_at	D80948	1738 D81048_at	#N/A	#N/A	150.18	149.32	51.77	86.08	85.08	39.11			

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	replication factor C	fold change in hcc		hcc sample set 2:		hcc sample set 2:		normal set 2:		normal set 2:	
				set 2	p value	Mean	Median	Mean	Std Dev	Mean	Median	Mean	Median
rc_F04320_s_at	F04320	1786	(activator 1) 4 (37kD)	6.29	0.00042	156.76	122.53	109.02	14.92	17.26	9.79		
rc_H14617_at	H14617	1884	EST	#N/A	#N/A	143.86	147.93	66.03	133.9	150.35	53.38		
rc_H26763_at	H26763	1907	EST	#N/A	#N/A	408.05	321.65	219.8	409.85	391.85	155.84		
rc_H68794_at	H68794	1984	EST	3.67	0.00327	215.75	176.78	110.42	65.56	54	51.09		
rc_H78211_at	H78211	2001	EST	7.5	0.02674	285.43	307.06	261.02	-115.95	-129.18	70.22		
rc_H95566_f_at	H95566	2050	EST	#N/A	#N/A	136.58	143.31	26.27	74.11	89.04	126.61		
rc_H99870_at	H99870	2082	EST	#N/A	#N/A	92.81	94.93	33.98	53.86	61.17	29.86		
rc_N62487_at	N62487	2591	EST	#N/A	#N/A	56.6	52.26	33.75	13.89	16.02	8.53		
rc_N67815_f_at	N67815	2627	EST	3.84	0.00439	351.55	356.17	99.35	104.07	151.77	86.01		
rc_N69084_l_at	N69084	2643	EST	3.11	0.0094	233.32	208.16	169.31	72.13	67.7	49.99		
rc_N73278_at	N73278	2672	EST	#N/A	#N/A	77.72	71.59	49.4	25.36	19.22	26.85		
rc_R06251_f_at	R06251	2764	tumor protein D52-like 2 carbohydrate sulfate Gal-6)	4.88	0.03097	466.88	341.39	380.43	74.25	66.72	64.11		
rc_R15740_at	R15740	2791	sulfotransferase 1	3.36	0.00268	117.43	100.03	64.73	31.77	21.3	33.53		
rc_R24507_at	R24507	2802	EST	#N/A	#N/A	31.61	16.41	30.69	3	3.45	5.62		
rc_R27296_f_at	R27296	2807	EST	3.41	0.00309	77.08	67.51	39.42	8.27	11.07	7.26		
rc_R30931_at	R30931	2810	EST	#N/A	#N/A	54.19	57.09	29.34	17.58	13.67	14.21		
rc_R45994_f_at	R45994	2867	EST	6.48	0.00358	730.52	598.82	420.14	145.88	160.69	163.03		
rc_R70253_at	R70253	2945	EST	3.38	0.03125	99.7	88.01	87.93	-9.59	-0.47	30.83		
rc_R72886_s_at	R72886	2956	KIAA0422 protein	5.5	0.00091	564.05	473.4	207.71	126.66	121.18	116.07		
rc_R96924_s_at	R96924	3001	EST	7.04	0.00012	336.8	329	106.3	51.01	52.94	54.09		
rc_T15852_f_at	T15852	3062	EST	5.21	0.00642	168.18	134.42	120.18	-7.59	7.36	51.48		
rc_T16983_s_at	T16983	3074	polyadenylation specific factor 4, 30kD subunit	4.23	0.0106	262.26	268.2	155.86	65.64	45.67	74.28		

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	RNA (guanine-7-)	fold change		hcc		hcc		hcc		normal		normal	
				In hcc set 2	p value	sample set 2: Median	sample set 2: Std Dev	sample set 2: Mean	sample set 2: Std Dev	set 2: Median	set 2: Std Dev	set 2: Mean	set 2: Std Dev	set 2: Median	set 2: Std Dev
rc_T33865_f_at	T33865	3110	methyltransferase	#N/A	#N/A	29.73	32.86	22.11	-0.26	2.33	8.15				
rc_T66935_at	T66935	3179	EST	3.01	0.00123	181.34	189.67	61.49	66.8	52.94	42.32				
rc_T95057_f_at	T95057	3259	EST	6.46	0.00613	229.11	188.71	174.46	7.13	15.37	37.2				
rc_W45320_f_at	W45320	3523	KRAB-associated protein 1	10.05	0.00002	365.22	345.46	124.13	-2.52	25.03	112.32				
AF006041_at	AF006041	1549	death-associated protein 6	#N/A	#N/A	174.22	170.16	37.64	74.91	58.55	50.31				
D00596_at	D00596	1590	thymidylate synthetase	5.58	0.0098	200.17	128.11	170.5	20.16	20.43	12.43				
D38491_at	D38491	1653	KIAA0117 protein	#N/A	#N/A	47.67	52.03	21.01	20.77	20.88	17.43				
D63486_at	D63486	1712	KIAA0152 gene product	3.56	0.00063	277.42	248.24	99.25	84.6	95.61	45.48				
			minichromosome maintenance deficient												
D84557_at	D84557	1749	(mls5, S. pombe) 6	3.97	0.0017	184.48	132.11	125.74	37.22	43.12	28.15				
D86957_at	D86957	1754	KIAA0202 protein	3.08	0.02949	91.22	73.14	89.89	14.7	12.7	6.29				
D86972_at	D86972	1755	KIAA0218 gene product	#N/A	#N/A	68.56	66.54	32.32	34.58	32.05	21.82				
D90097_at	D90097	1768	amylase, alpha 2B; pancreatic	#N/A	#N/A	41.19	37.49	21.85	6.55	11.44	15.06				
L29218_at	L29218	2190	CDC-like kinase 2	3.82	0.00035	155.42	142.58	76.28	35.11	41.27	26.41				
L38696_at	L38696	2208	RNA-binding protein (autoantigenic)	#N/A	#N/A	127.32	114.91	62.34	60.18	58.55	24.77				
M11749_at	M11749	2240	Thy-1 cell surface antigen	#N/A	#N/A	83.1	65.86	64.52	26.05	28.95	20.56				
M25753_at	M25753	2308	cyclin B1	#N/A	#N/A	44.14	30.96	40.36	-0.8	3.03	15.35				
M32334_at	M32334	2333	intercellular adhesion molecule 2	#N/A	#N/A	95.04	92.33	67.51	42.19	41.31	27.33				
M55210_at	M55210	2353	laminin, gamma 1 (formerly LAMB2)	3.47	0.02551	137.63	115.85	102.71	27.07	29.17	12.36				
M61916_at	M61916	2372	laminin, beta 1	3.18	0.01171	75.1	67.4	61.41	7.19	7.98	8.98				

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	stress-induced-		fold change In hcc set 2:	p value	sample set 2: Mean	sample set 2: Median	hcc sample set 2: Mean	hcc sample set 2: Median	normal set 2: Mean	normal set 2: Median	normal set 2: Std Dev	
			fold	change In hcc set 2:										
M86752_at	M86752	2412	phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	5.15	0.02881	216.51	248.21	192.98	8.67	20.63	39.03			
M87339_at	M87339	2415	replication factor C (activator 1) 4 (37kD)	4.59	0.00116	110.39	82.61	79.29	4.26	9.92	16.79			
M94250_at	M94250	2426	mildine (neurite growth- promoting factor 2)	9.86	0.02104	690.32	193.74	1414.43	-155.4	-175.43	101.89			
S72904_at	S72904	3031	antigen 1	#N/A	#N/A	29.33	29.21	18.34	11.53	12.85	7.55			
S78187_at	S78187	3036	cell division cycle 25B	4.83	0.00547	143.52	115.3	109.13	3.36	-1.2	26.9			
S78569_at	S78569	3037	laminin, alpha 4	#N/A	#N/A	25.79	26.91	21.66	6.3	7.6	9.38			
U38847_at	U38847	3357	TAR (HIV) RNA-binding protein 1	#N/A	#N/A	83.43	70.23	66.3	15.7	17.43	10.2			
U51477_at	U51477	3384	diacylglycerol kinase, zeta (104kD)	#N/A	#N/A	73.85	61.64	31.81	36.35	36.29	23.02			
U59321_at	U59321	3398	DEAD/H (Asp-Glu-Ala- Asp/His) box polypeptide 17 (72kD)	3.12	0.02469	84.5	98.2	70.13	3.1	-1.83	19.73			
U66661_at	U66661	3406	gamma-aminobutyric acid (GABA) A receptor, epsilon	3.55	0.0045	97.79	83.66	61.79	16.58	14.81	11.96			
U93237_mna2_at	U93237	3462	multiple endocrine neoplasia I	#N/A	#N/A	84.78	93.3	24.25	45.63	45.39	17.66			
X92106_at	X92106	3822	bleomycin hydrolase	#N/A	#N/A	56.15	48.48	36.93	4.73	3.77	11.78			

Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	p value	fold change	hcc	hcc	hcc	sample set 2:	sample set 2:	normal set 2:	normal set 2:	normal set 2:	normal set 2:
				in hcc	set 2	sample set 2:	Median	Std Dev	Mean	Median	Std Dev	Median	Std Dev
		tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	#N/A	82.96	83.94	15.05	23.4	33.5	24.15				
X92762_at	X92762	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	#N/A	47.87	47.61	18.08	18.99	22.48	13.31				
Y09216_at	Y09216	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	#N/A	86.89	70.61	47.65	38.18	47.33	23.06				
M69013_at	M69013	RAD23 (<i>S. cerevisiae</i>) homolog A	#N/A	97.12	98.23	25.66	37.18	32.35	28.04				
AD0000092_cds7_s_at	AD0000092	small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) myosin, light polypeptide 1, alkali; skeletal, fast protein kinase, interferon-inducible double stranded RNA dependent Iduonidase, alpha-L-a disintegrin and metalloproteinase domain	#N/A	122.45	134.9	49.51	42.22	41.24	17.18				
X04654_s_at	X04654	#N/A	#N/A	60.22	49.75	54.83	-2.19	-4.38	11.56				
M31211_s_at	M31211	#N/A	#N/A	#N/A	#N/A	121.95	72.58	41.88	24.48				
U50648_s_at	U50648	RNA dependent	#N/A	214.34	192.86	122.38	105.38	92.58	43.12				
M74715_s_at	M74715	Iduronidase, alpha-L-	#N/A	122.69	121.95	72.58	41.88	24.48	43.99				
U41767_s_at	U41767	a disintegrin and metalloproteinase domain 15 (metarginidin)	#N/A	196.76	147.11	113.93	83.03	66.93	68.33				
M12125_at	M12125	tropomyosin 2 (beta)	7.13	0.0004	174.25	183.97	95.24	13.01	16.33	11.64			
U20499_at	U20499	sulfotransferase family 1A, phenol-preferring, member 3	#N/A	141.35	126.33	135.57	48.34	54.37	24.69				

Table 8B: Genes and ESTs expressed only in normal liver compared to hepatocellular carcinoma.

Affy ID	Genbank Seq ID	Known Gene Name	hcc change	p value	hcc sample		hcc sample		normal sample		normal sample	
					set 2: Mean	set 2: Std Dev	set 2: Mean	set 2: Std Dev	set 2: Median	set 2: Std Dev	set 2: Median	set 2: Std Dev
rc_AA010205_at	AA010205	AA013095_s_at	AA013095	33	channel, shaker-related potassium voltage-gated	#N/A	5.71	0.00014	26.95	20.06	32.19	187.55
rc_AA046747_at	AA046747	AA046747	114	EST	4.77	0.00023	-0.57	3.68	23.81	113.78	88.54	66.41
rc_AA074885_at	AA074885	macrophage receptor with	161		10.88	0.00087	35.67	58.01	44.34	652.03	761.74	300.57
rc_AA099225_at	AA099225		206	EST	6.59	0.00064	10.9	9.75	15.11	212.68	163.45	194.31
rc_AA253410_at	AA253410	AA253410	564	EST	#N/A	#N/A	3.66	1.48	10.67	49.37	26.82	45.2
rc_AA281796_at	AA281796	AA281796	650	mannose-P-dolichol utilization	#N/A	#N/A	95.74	105.86	45.46	170.88	165.02	41.87
rc_AA282541_at	AA282541	AA282541	661	EST	#N/A	#N/A	17.21	11.75	13.38	31.31	29.9	13.53
rc_AA285053_at	AA285053	AA285053	681	EST	5	0.00718	36.49	20.15	49.24	238.16	242.27	169.12
rc_AA287566_at	AA287566	AA287566	690	KIAA0187 gene product	6.99	0.00023	18.67	14.05	35.71	246.24	201.66	228.64
rc_AA404248_at	AA404248	AA404248	847	EST	#N/A	#N/A	24.05	30.59	15.83	40.92	35.06	17.49
rc_AA448002_at	AA448002	putative type II membrane	1113		14.14	0	39.9	38.99	13.33	594.13	528.63	282.58
rc_AA460661_at	AA460661	AA460661	1229	EST	5.46	0.00151	20.05	8.57	39.04	184.62	198.21	108.17
rc_AA487576_at	AA487576	AA487576	1357	EST	#N/A	#N/A	11.67	2.42	27.75	26.05	25.27	11.13
rc_AA621235_at	AA621235	AA621235	1517	EST	#N/A	#N/A	65.79	68.63	35.33	114.75	113.36	65.35
rc_F09979_at	F09979	F09979	1809	EST	#N/A	#N/A	61.21	6.31	128.69	226.47	116.41	288.21
rc_F10380_at	F10380	butyrobetaine (gamma), 2-oxoglutarate dioxygenase			#N/A	#N/A	43.64	47.09	18.15	106.49	93.71	83.35
rc_H57056_at	H57056	H57056	1953	EST	#N/A	#N/A	-1.79	-7.37	11.38	35.07	38.32	17.88
rc_H58673_at	H58673	H58673	1959	EST	15.49	0.00002	34.96	26.37	38.53	652.47	677.55	376.36
rc_H59136_at	H59136	H59136	1962	EST	6.63	0.00033	33.12	21.17	42.92	250.23	229.94	129.12
H66367_at	H66367	H66367	1977	EST	3.84	0.00133	37.14	35.15	26.61	155.38	149.31	70.77
H72650_at	H72650	H72650	1994	EST	#N/A	#N/A	78.97	93.74	40.9	122	125	42.24
rc_H87765_at	H87765	H87765	2017	KIAA0626 gene product	3.94	0.00123	10.11	10.07	4.23	94.26	93.78	60.64
M10943_at	M10943	M10943	2234	metallothionein 1F (functional)	6.23	0.00007	35.67	28.76	22.4	217.65	186.71	86.73
M30185_at	M30185	M30185	2321	cholesteryl ester transfer protein,	3.82	0.00131	-15.66	-12.63	23.86	93.07	86.04	61.35
M63967_at	M63967	M63967	2378	aldehyde dehydrogenase 5	3.88	0.00274	40.43	30.04	29.05	164.38	178.74	87.39

Table 8B. Genes and ESTs expressed only in normal liver compared to hepatocellular carcinoma.

Affy ID	Genbank Seq ID	Known Gene Name	hcc change	p value	hcc			hcc			normal set 2: Median	normal set 2: Std Dev
					sample set 2:							
rc_N22404_at	N22404	2450 EST	3.44	0.02267	56.69	35.82	73.26	193.63	130.09	162.83		
rc_N34919_at	N34919	2499 EST	#N/A	#N/A	19.32	19.72	14.37	52.96	44.23	24.23		
rc_N54604_at	N54604	2570 EST	#N/A	#N/A	45.27	14.34	81.45	133.06	119.1	109.95		
rc_N65959_at	N65959	2612 EST	3.38	0.00785	37.8	28.94	31.45	142.87	149.26	79.26		
rc_N67105_at	N67105	2624 EST	4.69	0.00194	12.46	10.45	12.64	143.36	102.9	121.4		
rc_N69114_at	N69114	2644 nuclear receptor subfamily 1, collectin sub-family member 10	#N/A	#N/A	12.69	5.95	15.01	72.29	73.28	57.34		
rc_N74624_at	N74624	2688 orosomucoid 1	#N/A	#N/A	39.43	35.17	24.21	71.81	62.09	43.57		
N99542_at	N99542	2747	3.53	0.00607	61.09	67.97	39.3	226.06	187.68	146.11		
rc_R09053_at	R09053	2783 EST	3.45	0.03074	64.12	36.33	102.03	186.87	204.61	113.19		
rc_R73816_at	R73816	2961 EST	7.05	0.01287	35.12	13.76	100.6	462.31	374.67	450.91		
rc_R99591_at	R99591	3016 receptor cysteine rich family	7.41	0.00043	124.14	139.76	50.35	1035.39	904.92	691.83		
rc_T58756_at	T58756	3156 EST	16.61	0	-1.02	1.06	24.36	390.04	386.76	164.41		
T68083_at	T68083	3185 short-chain	#N/A	#N/A	96.34	59.71	104.53	263.22	280.22	136.48		
rc_T68711_at	T68711	3188 EST	35.98	0.0003	29.03	-33.95	176.15	1388.67	1074.67	890.91		
rc_W48860_at	W48860	3537 EST	#N/A	#N/A	37.25	31.7	27.5	52.69	41.31	21.1		
rc_W78093_at	W78093	3601 X-prolyl aminopeptidase (aminopeptidase P) 2,	#N/A	#N/A	408.58	397.88	102.27	518.77	518.8	211.32		
rc_W85890_at	W85890	3623 EST	#N/A	#N/A	60.91	60.47	23.73	70.98	66.52	24.66		
rc_W90018_f_at	W90018	3642 EST	#N/A	#N/A	21.51	1.31	56.9	59.32	53.19	41.68		
X54380_at	X54380	3730 pregnancy-zone protein	7.71	0.00069	15.11	8.07	27.07	274.41	255.4	203.47		
Z48475_at	Z48475	3943 glucokinase (hexokinase 4) subfamily A (Cys-Cys), member	4.6	0.01693	65.99	51.37	146.72	305.23	239.52	155.98		
Z49269_at	Z49269	3945 14	7.24	0.01047	138.63	66.95	201.93	526.13	532.29	166.67		

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	p Value	metastatic: Mean	metastatic: Median	metastatic: Std Dev	normal			normal		
								fold change	in metas	set 2: Mean	set 2: Median	set 2: Std Dev	
rc_AA007160_at	AA007160	16	EST	0.01035	171.32	175.07	138.03	6	0.01035	9.1	8.6	12.54	
rc_AA009913_at	AA009913	21	diphtheria toxin biosynthesis required for diphthamide biosynthesis (Saccharomyces)-like 2	#N/A	69.53	81.03	27.69	28.79	0.00602	1157.47	1448.16	18.22	
rc_AA011134_at	AA011134	29	EST	#N/A	566.78	566.78	-72.57	DKFZP434G032			-51.2	13.51	
rc_AA024482_at	AA024482	45	protein	#N/A	207.37	118.58	-1.3	AA026030	11.01	0.01649	230.63	69.3	
rc_AA026030_at	AA026030	53	EST	#N/A	566.65	284.32	3.02	tyrosyl-tRNA synthetase			4.66	13.6	
rc_AA026270_at	AA026270	56	AA026270	#N/A	201.1	224.51	3.41	glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)	#N/A	39.84	76.85	40.87	
rc_AA035540_at	AA035540	81	AA040465	#N/A	161.91	125.35	13.59	rc_AA040465_at	3.25	0.00146	72.19	12.27	
rc_AA043944_at	AA043944	100	AA053033	#N/A	52.9	29.13	45.53	rc_AA043944_at			47.15	8.96	
rc_AA053033_at	AA053033	124	EST	#N/A	212.61	46.43	3.15	rc_AA053033_at	7.83	0.00379	135.28	5.48	
rc_AA053102_s_at	AA053102	125	cadherin 17, L1 cadherin (liver-Intestine)	#N/A	34.37	34.37	3.41	rc_AA053248_i_at			3.69	7.26	
rc_AA053248_i_at	AA053248	126	EST	#N/A	1595.15	1053.3	-1.28	rc_AA053660_at	7.01	0.00003	1053.3	19.74	
rc_AA053660_at	AA053660	128	EST	#N/A	1573.49	1340		rc_AA055805_s_at	15.98	0.00003	820.5	341.06	
rc_AA055805_s_at	AA055805	132	EST	#N/A	1270.03	1270.03		rc_AA055805	42.83	0.00142	1026.97	304.8	
rc_AA055805								rc_AA055805			95.24	42.99	
rc_AA055805								rc_AA055805			1179.12	189.89	
rc_AA055805								rc_AA055805			-10.85	20.27	

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change		metastatic		metastatic:		normal		normal	
				In metas	p value	Mean	Median	Median	Std Dev	Mean	Std Dev	set 2: Median	set 2: Std Dev
rc_AA055811_s_at	AA055811	133	glycoprotein A33 (transmembrane)	6.86	0.02152	236.18	196.53	171.06	14.84	17.82	17.5		
rc_AA055896_at	AA055896	135	collagen, type V, alpha 1	18.16	0.00146	540.67	538.43	382	-3.14	-5.8	33.88		
rc_AA084343_at	AA084343	178	EST	#N/A	#N/A	133.86	126.19	19.99	84.58	76.82	41.45		
			cardioembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	50.88	0.00081	1405.2	1264.79	1137.97	-17.03	-22.23	16.43		
rc_AA100719_s_at	AA100719	212	vaccinia related kinase 1	#N/A	#N/A	25.08	24.98	13.02	8.54	8.02	2.59		
rc_AA12979_s_at	AA12979	225	mitotic spindle coiled-coil related protein	#N/A	#N/A	74.58	89.38	66.52	22.91	13.67	29.42		
rc_AA115979_at	AA115979	232	EST	#N/A	#N/A	42.91	33.83	16.2	26.42	28.92	9.81		
rc_AA126041_at	AA126041	244	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	6.59	0.03706	332.45	208.85	296.68	-29.54	-28.71	104.37		
AA127712_at	AA127712	255											
rc_AA128553_f_at	AA128553	260	EST	#N/A	#N/A	87.35	102.82	24.17	114.91	108.16	30.28		
rc_AA131162_s_at	AA131162	266	EST	4.68	0.000442	117.43	123.78	39.05	11.86	13.57	19.83		
rc_AA134968_at	AA134968	289	EST	12.11	0.00079	322.34	208.47	256.66	10.04	7.96	15.53		
rc_AA150053_at	AA150053	327	EST	3.71	0.00102	309.61	304.16	82.48	101.87	88.37	73.73		
rc_AA151428_s_at	AA151428	335	matrix metalloproteinase 23B	7.15	0.00056	174.77	131.66	104.51	3.23	10.67	24.39		
rc_AA156243_at	AA156243	340	serine protease, umbilical endothelium	41.44	0.00139	1255.4	547.15	1189.26	9.32	11.44	9.39		

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic:			metastatic:			normal		
			#N/A	p value	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev	set 2: set 2:
rc_AA157857_s_at	AA157857	keratin 19	#N/A	2728.74	2917.98	1076.95	-13.21	-14.4	15.84					
rc_AA159525_at	AA159525	EST	49.39	0.00062	1309.05	1107.08	965.67	-32.72	-28.32	20.11				
rc_AA161043_at	AA161043	tetraspan 1	18.8	0.00015	1477.19	932.02	1467.59	70.82	58.62	42.88				
rc_AA171760_at	AA171760	EST	17.86	0	645.43	578.38	312.37	28.03	16.24	57.21				
rc_AA179787_at	AA179787	polyglutamine binding protein 1	6.44	0.00206	191.33	171.71	138.9	-11.56	-12.46	42.46				
rc_AA179845_at	AA179845	EST	5.77	0.01414	280.06	335.41	172.62	37.43	37.69	14.87				
rc_AA181600_at	AA181600	EST	5.38	0.03316	166.88	94.16	153.49	-40.51	-47.81	24.34				
rc_AA196790_at	AA196790	EST	7.64	0.00287	239.45	275.18	142.37	22.91	26.8	10.54				
rc_AA211483_at	AA211483	EST	44.07	0.00175	1300.23	1303.61	1051.58	-29.25	-34.99	17.49				
rc_AA227926_at	AA227926	EST	6.81	0.01701	228.91	120.1	243.92	16.24	14.21	6.86				
rc_AA232508_at	AA232508	EST	#N/A	464	533.98	266.87	170.48	156.89	104.75					
		general transcription factor III C, polypeptide 1 (alpha subunit, 220kD)	#N/A	#N/A	56.54	43.91	22.15	28.32	31.59	25.36				
rc_AA233290_at	AA233290	EST	23.72	0.00018	607.06	420.34	366.53	-3.47	1.73	30.91				
rc_AA234096_at	AA234096	EST	#N/A	#N/A	36.98	39.47	12.81	6.21	6.79	19.99				
rc_AA234346_at	AA234346	EST	3.89	0.03524	116.26	75.37	105.77	-1.86	-4.2	16.67				
rc_AA234362_at	AA234362	survival of motor neuron protein interacting protein 1	#N/A	#N/A	56.37	42.6	34.73	12.96	16.93	12.99				
rc_AA234365_at	AA234365	EST	#N/A	#N/A	68.33	53.21	21.55	49.66	39.76	42.06				
rc_AA234706_at	AA234706	EST	9.17	0.00005	189.42	161.88	57.05	-18.19	-19.06	14.8				
rc_AA235707_at	AA235707	EST												
rc_AA236533_s_at	AA236533	ecotropic viral integration site 1	4.01	0.02982	106.15	76.05	78.18	-16.45	-14.04	8.52				
rc_AA243173_at	AA243173	EST	8.75	0.00003	384.86	482.53	162.08	41.66	40.74	27.31				
rc_AA252994_at	AA252994	apoptosis inhibitor 4 (survivin)	3.55	0.00075	152.63	140.53	31.01	50.23	40.59	35.61				

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change		metastatic:		metastatic:		normal	
				In metast	p value	Mean	Median	Std Dev	Mean	Median	Std Dev
AA253330_s_at	AA253330	562	protein complex 1, adaptor-related	3.87	0.00708	219.95	186.12	141.92	47.32	51.59	30.28
rc_AA253473_at	AA253473	567	gamma 1 subunit	15.23	0.00171	375.2	435.68	216.18	-4.38	-3.19	12.35
rc_AA255566_at	AA255566	570	EST	#N/A	#N/A	63.43	65.2	30.17	16.18	14.38	13.17
rc_AA256642_at	AA256642	582	EST	11.17	0.00035	266.31	275.43	135.85	0.78	-1.34	15.74
rc_AA258836_at	AA258836	601	WW domain binding protein 4 (formin binding protein 21)	#N/A	#N/A	41.9	44.58	13.6	26.08	23.64	10.4
rc_AA262943_at	AA262943	611	EST	13.42	0.00234	430.7	207.29	511.01	-1.08	-6.93	19.06
rc_AA281214_s_at	AA281214	643	neuroblastoma-amplified protein	#N/A	#N/A	130.98	133.63	68.42	69.89	53.91	39.31
rc_AA282505_at	AA282505	659	EST	#N/A	#N/A	461.54	478.83	622.39	-41.45	-17	98.17
rc_AA291259_at	AA291259	697	putative G protein-coupled receptor	#N/A	#N/A	112.28	45.1	113.44	1.53	1.88	6.06
AA291456_s_at	AA291456	700	EST	3.96	0.03633	1808.4	1273.75	1481.84	671.21	509.58	629.13
rc_AA292765_at	AA292765	712	ZW10 interactor	7.14	0.02623	230.83	166.72	232.16	11.33	18.29	13.27
rc_AA292931_at	AA292931	715	EST	3.97	0.00067	230.65	260.43	79.42	57.32	61.89	18.62
AA295819_s_at	AA295819	722	EST	8	0.01793	230.14	251.43	146.89	-14.93	-20.8	19.72
rc_AA331393_at	AA331393	739	EST	16.73	0.00848	600.02	315.98	598.52	5.08	3.88	9.43
rc_AA335191_f_at	AA335191	741	creatine kinase, brain	47.35	0.00419	3540.65	3971.43	3135.19	43.84	33.21	43.52
rc_AA349792_s_at	AA349792	759	mutY (E. coli) homolog	#N/A	#N/A	525.17	553.97	245.2	221.5	212.24	98.86
rc_AA372018_at	AA372018	768	EST	14.3	0.00178	363.44	220.03	261.04	-2.44	-3.09	8.36
AA372630_s_at	AA372630	769	differentially expressed in hematopoietic lineages	25.49	0.01743	2094.32	436.62	3873.61	6.67	4.87	7.16

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in metas				metastatic: mean median				normal: mean median				normal: mean median			
			p value	Mean	Median	Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev			
AA384184_s_at	AA384184	DKFZP586B0519	3.38	0.01209	476.17	411.64	148.86	181.02	188.54	135.4								
rc_AA394121_at	AA394121	protein laminin receptor 1 (67kD, ribosomal protein SA)	23.78	0.00099	788.51	677.33	612.74	0.21	-8.38	31.59								
rc_AA398908_at	AA398908	EST	38.69	0.01089	1678.58	1796.68	1500.48	-174.29	-216.08	104.42								
rc_AA399226_at	AA399226	tight junction protein 3 (zona occludens 3)	3.59	0.02002	89.54	78.97	63.98	-5.01	-6.48	11.33								
		tumor suppressor deleted in oral cancer-related 1	#N/A	#N/A	384.12	271.95	444.06	120.58	93.29	109.41								
rc_AA404597_at	AA404597	EST	854	#N/A	624.37	495.56	274.8	379.26	336.33	167.43								
rc_AA405715_at	AA405715	hypothetical protein	862	0.00898	152.23	138.92	96.78	24.47	27.3	11.75								
rc_AA406542_at	AA406542	EST	878	0.00724	230.18	170.94	206.8	-1.99	1.49	12.75								
rc_AA410469_at	AA410469	EST	883	0.00103	337.03	250.11	264.1	50.51	42.79	60.18								
rc_AA419217_at	AA419217	DKFZP586E1422 protein	923	6.77	0.00045	276.53	215.37	172.25	36.93	36.7	21.88							
		anterior gradient 2 (Xenopus laevis) homolog	56.3	0.0041	2556.78	792	3323.39	14.22	15.72	6.54								
rc_AA421562_at	AA421562	EST	934	0.03418	828.27	598.22	800.79	39.48	34.98	23.29								
rc_AA422086_at	AA422086	cytochrome P540 family member	938	10.71														
rc_AA422150_at	AA422150	predicted from ESTs	939	17.14	0.00108	664.26	609.99	475.91	28.76	27.53	22.47							
rc_AA424487_at	AA424487	EST	945	38.41	0.00002	2689.32	1863.02	1900.51	67.92	61.95	46.24							
rc_AA424881_at	AA424881	EST	949	6.3	0.00556	158.13	155.45	82.63	-16.85	-22.15	20.49							
rc_AA425279_at	AA425279	quiescin Q6	951	6.15	0.00083	221.93	181.8	167.44	18.33	22.33	44.81							

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change		metastatic: In metas		metastatic: Median		metastatic: Std Dev		normal: set 2:		normal: set 2:	
				p Value	In metas	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean
rc_AA425401_at	AA425401	954	yeast homolog	3.22	0.00625	246.6	166.4	175.99	76.4	78.33	43.72	49.3	52.2	4.75	
rc_AA425852_i_at	AA425852	958		4.8	0.03874	149.8	125.7	128.03	7.02	5.22					
rc_AA427460_s_at	AA427460	972	ATP-binding cassette, sub-family F (GCN20), member 2	#N/A	215.08	135.22	216.95	92.5	83.63	49.3					
AA427468_s_at	AA427468	973	claudin 4	84.43	0	5646.4	5344.98	1581.19	72.58	64.85	87.74				
rc_AA427636_at	AA427636	976	EST	19.23	0.00145	511.98	500.83	299.69	6.19	3.7	15.84				
rc_AA429009_at	AA429009	994	serine protease inhibitor, Kunitz type 1	30.04	0.00001	1010.32	1100.19	472.23	-2.97	-24.67	62.21				
rc_AA429890_s_at	AA429890	1004	cisplatin resistance associated	12.51	0.00053	1225.72	590.09	992.47	90.02	67.23	59.35				
rc_AA430674_at	AA430674	1018	EST	15.11	0.00293	454.82	306.15	378.36	-71.57	-82.03	59.56				
rc_AA436616_at	AA436616	1056	EST	3.18	0.04402	79.96	91.35	62.83	-0.73	3.24	15.36				
rc_AA442763_at	AA442763	1072	cyclin B2	5.09	0.02168	136.16	109.91	91.52	-14.64	-15.1	13.08				
rc_AA443316_s_at	AA443316	1075	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	4.13	0.01729	191.06	173.3	113.42	40.07	41.12	32.54				
rc_AA443941_at	AA443941	1085	tumor suppressing subtransferable candidate 1	3.57	0.01685	137.02	138.22	83.35	31.09	34.9	16.61				
rc_AA447687_at	AA447687	1104	EST	11.42	0.00362	306.28	178.65	244.12	-16.27	-14.45	8.55				
rc_AA447991_at	AA447991	1112	EST	4.99	0.00173	279.79	234.63	161.24	64.49	40.73	53.34				
rc_AA449456_at	AA449456	1126	EST	6.29	0.00087	847.4	775.81	377.99	160.93	178.76	112.71				
rc_AA451877_at	AA451877	1138	EST	8.63	0.00489	239.55	157.3	244.02	-27.28	-27.59	18.28				
rc_AA454597_s_at	AA454597	1166	EST	3.63	0.0067	268.15	274.94	167.72	66.6	57.29	23.41				

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change			metastatic:			metastatic:			normal				
				In metas	p value	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev	set 2: mean	set 2: median	set 2: std dev
AA454908_s_at	AA454908	1171	KIAA0144 gene product	9.3	0.00539	320.03	253.32	238.5	-33.7	-46.73	73.56						
rc_AA457235_at	AA457235	1200	EST	#N/A	#N/A	481.26	138.32	573.73	11.06	17.32	15.26						
rc_AA459254_at	AA459254	1211	EST	5.36	0.0259	403.69	194.85	401.21	51.84	43.51	37.57						
rc_AA460666_at	AA460666	1231	EST	#N/A	#N/A	56.19	58.13	26.29	-24.55	-17.23	20.98						
rc_AA463861_at	AA463861	1251	EST	24.79	0.00096	672.22	311.71	641.54	-22.02	-20.04	16.5						
rc_AA464962_at	AA464962	1264	EST	#N/A	#N/A	61.02	56.4	30.98	20.99	14.37	19.64						
rc_AA465342_at	AA465342	1271	EST	#N/A	#N/A	113.36	100.15	87.62	30.07	33.06	23.97						
rc_AA465660_at	AA465660	1273	LIM domain binding 1	#N/A	#N/A	171.26	118.15	103.39	124.59	105.93	56.71						
			tumor necrosis factor receptor superfamily, member 12 (translocating chain-association)														
rc_AA476749_s_at	AA476749	1286	membrane protein	#N/A	#N/A	53.23	44.04	18.16	25.5	29.62	11.96						
rc_AA477561_at	AA477561	1292	EST	#N/A	#N/A	160.87	104.95	133.7	63.83	76.56	37.87						
rc_AA478556_at	AA478556	1303	EST	#N/A	#N/A	172.35	136.55	120.49	143.25	134.62	109.1						
rc_AA482546_s_at	AA482546	1336	KIAA0124 protein	4.41	0.00604	181.72	113.91	140.73	38.26	30.26	32.72						
			chromosome 6 open reading frame 1														
rc_AA491208_at	AA491208	1388	KIAA0530 protein	#N/A	#N/A	159.88	143.86	80.49	123.37	131.81	47.97						
rc_AA599244_at	AA599244	1448	EST	3.39	0.01246	77.48	78.85	37.98	7.71	6.06	7.11						
rc_AA599585_at	AA599585	1454	dipeptidase 1 (renal)	#N/A	#N/A	66.17	48.91	48.12	-12.47	-17.55	21.82						
rc_AA609013_s_at	AA609013	1477	EST	10.17	0.00109	1185.55	1222.89	634.13	114.31	98.91	75.22						
rc_AA609795_at	AA609795	1492	EST	#N/A	#N/A	74.38	34	77.76	-41.44	-45.5	28.82						
rc_AA620497_s_at	AA620497	1503	EST	#N/A	#N/A	147.72	165.83	66.02	95.91	76.7	80.33						
rc_AA620995_at	AA620995	1512	EST	3.74	0.03414	100.71	80.15	101.95	3.5	1.8	3.77						
rc_AA621277_at	AA621277	1520	EST	3.81	0.00194	81.18	74.81	30.84	-0.15	1.98	12.84						
AB002304_at	AB002304	1534	KIAA0306 protein	#N/A	#N/A	584.5	621.94	136.64	313.99	298.88	88.6						

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	fold change				metastatic:			metastatic:			normal		
			In metas	p value	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev	set 2: Median	set 2: Std Dev
AB002349_at	AB002349	1537 product	#N/A	#N/A	65.63	52.11	32.26	49.37	46.52	37.93					
AB006782_at	AB006782	1541 (galectin 9)	#N/A	#N/A	475.47	430.44	192.68	222.25	213.37	51.25					
AF003521_at	AF003521	1545 jagged 2	11.26	0.00008	426	330.95	309.91	15.48	-3.6	91.81					
C00808_s_at	C00808	1553 EST	#N/A	#N/A	122.57	118.32	53.36	91.65	87.87	32.51					
C14228_f_at	C14228	1567 EST	#N/A	#N/A	39.93	33.15	13.59	-0.51	2.85	8.61					
rc_C15078_i_at	C15078	1573 EST	#N/A	#N/A	115.08	73.82	91.34	26.22	31.14	60.2					
rc_C21248_at	C21248	1585 pituitary tumor-transforming 1	3.85	0.00456	100.24	96.81	47.17	-1.7	-11.27	28.49					
D13435_at	D13435	1605 phosphatidylinositol glycan, class F	#N/A	#N/A	80.8	88.58	41.56	34.85	41.76	18.11					
D14520_at	D14520	1613 basic transcription element binding protein 2	4.93	0.00004	151.12	135.19	57.24	25.67	17.28	25.67					
rc_D20906_at	D20906	1627 minichromosome maintenance deficient (S. cerevisiae) 2	5.18	0.02189	210.11	151.67	185.24	14.87	11.71	27.2					
D21063_at	D21063	1628 (mitothin)	3.83	0.00983	91.18	55.12	60.89	-51.33	-62.63	28.4					
D50914_at	D50914	1673 KIAA0124 protein	4.74	0.00752	116.55	91.64	89.27	-17.4	-17.86	16.97					
D63486_at	D63486	1712 KIAA0152 gene product	6.33	0.00078	543.91	676.55	287.16	84.6	95.61	45.48					
D63880_at	D63880	1715 KIAA0159 gene product	4.26	0.00253	93.03	103.26	41.4	-2.12	-4.45	9.38					
D79992_at	D79992	1724 KIAA0170 gene product	#N/A	#N/A	35.23	42.16	14.88	22	18.08	11.9					

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	fold change				metastatic:				normal			
			In meta	p value	Mean	Median	metastatic:	metastatic:	Mean	Median	set 2:	set 2:	Mean	Std Dev
D79997_at	D79997	KIAA0175 gene	#N/A	#N/A	55.25	42.49	53.87	8.57	6.15	13.07				
rc_D80710_f_at	D80710	product	7.08	0.00213	253.6	303.7	149.08	22.95	28.29	24.59				
rc_D80948_f_at	D80948	Integral type I protein	#N/A	#N/A	82.4	67.39	42.83	41.25	43.53	17.46				
rc_F03735_at	D83735	EST	10.42	0.00001	486.85	436.55	172.25	42.54	43.06	57.58				
		calponin 2												
		trinucleotide repeat												
		containing 11 (THR-associated protein, 230 kDa subunit)												
D83783_at	D83783	minichromosome maintenance deficient (miss5, <i>S. pombe</i>) 6	#N/A	#N/A	142.92	125.75	102.81	37.22	43.12	28.15				
		zinc finger protein 142 (clone pHZ-49)	#N/A	#N/A	40.84	34.37	13.36	33.34	33.07	21.13				
D84557_at	D84557	villin-like EST	4.18	0.00051	117.8	129.16	47.7	23.85	18.99	17.79				
D87073_at	D87073	KIAA0440 protein	#N/A	#N/A	199.08	170.47	83.95	178.42	195.54	58.6				
D88154_at	D88154	replication factor C (activator 1) 4 (37kD)	#N/A	#N/A	638.66	598.46	142.63	235.37	232.6	47.16				
rc_F02330_at	F02330	Kell blood group precursor (McLeod phenotype)	3.63	0.01119	90.37	115.96	49.41	14.92	17.26	9.79				
rc_F03811_f_at	F03811													
rc_F04320_s_at	F04320													
rc_F04531_s_at	F04531													
rc_F09394_s_at	F09394													
		22.89	0.01753	865.39	696.47	631.83	-49.72	-50.25	35.81					
rc_F09788_at	F09788	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	4.14	0.00003	104.92	112.31	27.67	19.92	20.29	13.83				

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change			metastatic:			metastatic:			normal				
				In metas	p value	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev	set 2: mean	set 2: median	set 2: std dev
rc_H03629_s_at	H03629	1834	desmin	#N/A		52.19	58.52	35.47	-1.96	-2.94	8.58						
rc_H09281_at	H09281	1863	EST	6	0.00966	147.11	187.25	71.67	-2.97	-0.54	11.7						
rc_H111760_f_at	H111760	1878	EST	#N/A	#N/A	70.59	62.53	58.16	9.96	8.19	11.54						
rc_H24269_s_at	H24269	1902	E74-like factor 4 (ets domain transcription factor)	#N/A	#N/A	51.79	47.58	24.25	15.19	16.8	12.36						
H43286_s_at	H43286	1929	gamma-aminobutyric acid (GABA) B receptor, 1	5.02	0.01972	377.04	222.91	315.96	57.02	63.58	24.25						
rc_H43646_at	H43646	1930	H2A histone family, member Y	4.6	0.00147	413.02	424.34	219.27	92.12	91.3	52.41						
H53657_s_at	H53657	1945	adenylate cyclase 3	3.98	0.0045	140.07	111.99	74.77	31.33	31.74	15.29						
rc_H57709_s_at	H57709	1956	ribosomal protein L31	#N/A	#N/A	47.56	34.17	56.68	4.55	2.44	52.46						
			solute carrier family 2 (facilitated glucose transporter), member 1														
rc_H58873_s_at	H58873	1961		57.98	0.00063	4996.66	4603.55	4107.24	69.89	70.74	58.94						
rc_H59617_at	H59617	1964	EST	3.3	0.04588	116.07	71.39	101	19.24	21.65	16.88						
rc_H78211_at	H78211	2001	EST	6.73	0.02488	211.51	183.81	208.45	-115.95	-129.18	70.22						
rc_H98657_at	H98657	2068	EST	#N/A	#N/A	179.15	192.17	32.25	111.2	84.74	128.92						
J04469_at	J04469	2111	creatine kinase, mitochondrial 1 (ubiquitous)	7.9	0.00705	212.04	143.89	162.12	-17.21	-18.81	12.68						

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change		metastatic: in metas		metastatic: median		metastatic: std dev		normal: set 2:		normal: set 2:	
				In	p value	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean
J05257_at	J05257	2118	dipeptidase 1 (renal)	12.02	0.02099	429.91	300.76	352.56	-21.05	-21.78	30.67				
J05272_at	J05272	2119	IMP (inosine monophosphate) dehydrogenase 1	#N/A	#N/A	269.89	205	173.64	126.69	106.27	82.73				
J05582_s_at	J05582	2121	mucin 1, transmembrane ribosomal protein S6 kinase, 90kD, polypeptide 1	5.39	0.00056	114	114.74	42.09	-6.01	-4.53	13.68				
L07597_at	L07597	2146	trefoil factor 3 (Intestinal)	#N/A	#N/A	36.09	29.39	44.43	-12.04	-10.72	11.97				
L08044_s_at	L08044	2149	tetracycline transporter-like protein matrix metalloproteinase 12 (macrophage elastase)	21.42	0.01674	2956.22	1618.2	3127.19	107.82	58.55	184.16				
L11669_at	L11669	2157	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase) endothelial cell protein C/activated protein C receptor RNA-binding protein (autoantigenic) protease, serine, 8	6.75	0.00101	218.77	261.77	115.8	26.26	25.92	17.48				
L23808_at	L23808	2179	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase) endothelial cell protein C/activated protein C receptor RNA-binding protein (autoantigenic) protease, serine, 8	6.18	0.02195	175.24	161.83	132.75	-9.99	-8.2	8.11				
L35035_at	L35035	2201	endothelial cell protein C/activated protein C receptor RNA-binding protein (autoantigenic) protease, serine, 8	#N/A	#N/A	64.36	69.69	40.9	11.52	12.58	6.43				
L35545_at	L35545	2202	endothelial cell protein C/activated protein C receptor RNA-binding protein (autoantigenic) protease, serine, 8	#N/A	#N/A	66.65	55.46	68.13	7.75	5.68	11.48				
L38896_at	L38896	2208	endothelial cell protein C/activated protein C receptor RNA-binding protein (autoantigenic) protease, serine, 8	3.7	0.00093	230.48	161.69	118.85	60.18	58.55	24.77				
L41351_at	L41351	2214	endothelial cell protein C/activated protein C receptor RNA-binding protein (autoantigenic) protease, serine, 8	6.34	0.01132	214.13	104.95	189.28	10.88	9.6	22.68				

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change			metastatic:			metastatic:			normal		
				In metas	P value	Mean	Median	Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	
M94345_at	M94345	2427	capping protein (actin filament), gelsolin-like	22.38	0.00003	503.47	539.15	179.05	-7.51	-10.35	22.75				
M94362_at	M94362	2428	lamin B2	#N/A	#N/A	175.16	154.32	75.52	79.2	81.73	34.64				
M94891_s_at	M94891	2429	pregnancy specific beta-1-glycoprotein 4, pregnancy specific beta-1-glycoprotein 7	#N/A	#N/A	221.09	197.74	80.32	178.23	166.98	61.33				
M95623_cds1_at	M95623	2431	hydroxymethylbilane synthase	#N/A	#N/A	67.65	72.44	22.29	6.67	0.88	24.92				
rc_N22015_at	N22015	2448	EST	46.61	0.00025	1225.51	887.65	1106.3	-5.3	-6.84	18.82				
rc_N35376_at	N35376	2501	EST	#N/A	#N/A	39.01	35.99	19.81	28.53	29.44	8.2				
rc_N49284_s_at	N49284	2537	v-myb avian myeloblastosis viral oncogene homolog	11.82	0.01981	510.82	523.45	423.41	-36.17	-50.08	50.71				
rc_N54265_s_at	N54265	2563	EST	#N/A	#N/A	45.56	44.98	19.91	17.71	26.43	25.36				
rc_N54395_at	N54395	2565	EST	#N/A	#N/A	49.95	46.84	48.26	-16.14	-17.71	6.65				
rc_N62675_s_at	N62675	2594	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16	3.61	0.04034	109.44	104.65	108.08	6.49	15.91	35.18				
rc_N63165_at	N63165	2598	EST	#N/A	#N/A	68.04	62.1	44.7	30.07	26.23	13.84				
rc_N64616_at	N64616	2611	EST	3.11	0.0074	68.89	75.8	32.12	-0.83	9.77	28.69				
rc_N66951_at	N66951	2621	EST	5.54	0.02442	451.16	432.45	381.81	59.83	75.27	32.75				
			solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2												
rc_N72116_s_at	N72116	2668	EST	9.01	0.00051	338.43	314.06	196.66	32.57	29.68	20.1				
rc_N73846_at	N73846	2680	EST	3.27	0.00012	78.37	79.7	20.06	14.43	14.3	17.21				

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in metas		metastatic: Mean		metastatic: Median		metastatic: Std Dev		normal set 2: Mean		normal set 2: Median		normal set 2: Std Dev	
			p value	in metas	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev
rc_N89670_at	N89670	EST	4.26	0.00002	115.98	108.4	29.79	3.16	-1.81	43.32						
rc_N92659_at	N92659	EST	#N/A	#N/A	31.19	37.23	14.14	5.91	4.05	5.63						
rc_N92734_at	N92734	EST	#N/A	#N/A	45.63	39.49	14.19	27.31	25.45	10.41						
rc_N93798_at	N93798	member 3	4.65	0.00118	557.51	523.56	229.03	139.69	122.61	84.93						
rc_R06251_f_at	R06251	tumor protein D52-like 2	5.57	0.00037	343.86	381.79	95.11	74.25	66.72	64.11						
rc_R06866_s_at	R06866	EST	5.18	0.00187	148.48	114.86	102.01	18.26	15.16	17.11						
rc_R26744_at	R26744	midline 1 (Optitz/BBB syndrome)	4.32	0.00532	112.54	90	76.53	-0.2	-3.06	24.42						
rc_R27296_f_at	R27296	EST	#N/A	#N/A	41.82	39.83	32.72	8.27	11.07	7.26						
rc_R33498_s_at	R33498	EST	41.34	0.00001	1839.74	1920.41	1082.84	46.45	33.01	43.64						
rc_R36109_at	R36109	EST	#N/A	#N/A	47.54	48.43	19.9	25.67	20.25	34.73						
rc_R36947_s_at	R36947	calcium channel, voltage-dependent, beta 3 subunit	4.11	0.00006	101.82	109.62	28.57	-0.61	0.94	37.6						
rc_R38511_s_at	R38511	protein similar to E.coli ydg and R.	5.19	0.00015	131.5	147.54	44.02	21.3	23.75	9.22						
rc_R39191_s_at	R39191	capsulatus nifR3 KIAA1020 protein	4.69	0.00456	130.93	145.31	62.13	17.46	18.33	16.04						
rc_R40057_at	R40057	prominin (mouse)-like 1	#N/A	#N/A	47.6	46.28	36.57	0.83	-0.8	7.91						
rc_R44479_at	R44479	KIAA0552 gene product	4.14	0.0181	97.01	105.95	60.51	7.08	5.99	7.62						
rc_R44817_at	R44817	EST	#N/A	#N/A	600.1	550.42	309.14	255.91	249.29	69.09						
rc_R49047_at	R49047	Fc fragment of IgG, low affinity IIIa, receptor for (CD16)	#N/A	#N/A	44.49	36.71	14.37	15.43	14.16	14.13						

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change			metastatic:			metastatic:			normal		
				In metas	p value	Mean	Median	Std Dev	set 2:	Median	Mean	Std Dev	set 2:	Median	Mean
rc_R54935_i_at	R54935	2903	ubiquitin specific protease 7 (herpes virus-associated)	#N/A	75.76	81.15	31.57	17.77	14	18.86					
rc_R55470_at	R55470	2904	EST	3.59	0.00515	256.38	225.69	138.22	75.29	73.42	53.04				
R56678_at	R56678	2908	EST	3.81	0.02242	98.37	78.38	75.74	2.67	5	5.82				
rc_R59093_at	R59093	2911	EST	#N/A	57.79	33.48	73.58	12.26	10.21	7.73					
rc_R63925_at	R63925	2929	EST	#N/A	70.52	60.93	15.36	49.82	52.73	13.77					
R69700_at	R69700	2943	EST	6.71	0.0021	387.34	393.81	94.86	79.33	67.85	129.97				
rc_R71395_at	R71395	2952	EST	10.42	0.00422	318.75	274.93	227.75	14.99	12.28	14.58				
R76363_at	R76363	2962	EST	#N/A	47.81	38.04	24.76	12.67	16.94	13.17					
rc_R85266_at	R85266	2977	EST	#N/A	53.4	54.53	25.44	48.68	39.83	33.9					
rc_R91819_at	R91819	2984	matrix metalloproteinase 12 (macrophage elastase)	8.95	0.0009	263.33	219.91	135.67	11.34	9.35	36.49				
rc_R92994_s_at	R92994	2990		11.05	0.00248	312.14	252.62	248.32	11.43	6.64	11.52				
rc_R95966_i_at	R95966	2997	EST	11.22	0.00682	482.68	436.3	446.39	-106.64	-160.75	127.91				
rc_R96924_s_at	R96924	3001	EST	6.18	0.03417	451.59	490.51	339.66	51.01	52.94	54.09				
S78187_at	S78187	3036	cell division cycle 25B	8.07	0.0009	198.51	218.04	74.52	3.36	-1.2	26.9				
rc_T03438_s_at	T03438	3043	EST	8.18	0.00032	300.09	229.6	218.02	31.03	28.88	15.86				
rc_T03541_at	T03541	3045	EST	#N/A	455.39	418.21	288.45	155.27	155.62	50.93					
rc_T15473_at	T15473	3058	muscle specific gene cleavage and polyadenylation specific factor 4, 30kD	5.81	0.02404	189.25	139.11	184.39	-5.65	-10.77	15.89				
rc_T16983_s_at	T16983	3074	subunit	5.23	0.00075	268.21	300.53	81.43	65.64	45.67	74.28				
rc_T25744_s_at	T25744	3092	EST	#N/A	#N/A	79.78	68.72	52.01	15.56	12.65	13.18				

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	In metas	p value	fold change			metastatic: metastatic:			normal: normal:		
						Mean	Median	Std Dev	Mean	Median	Std Dev	set 2: set 2:	Mean	Median
rc_T30193_s_at	T30193	3098	protease, serine, 8 (prostasin)	8.39	0.00043	1912.22	1228.46	1739.5	214.88	175.57	127.28			
rc_T30222_at	T30222	3100	EST	#N/A		35.41	34.75	27.14	8.47	9.56	17.71			
rc_T32108_at	T32108	3103	EST	6.96	0.00723	1095.16	593.52	923.47	148.09	152.11	92.06			
rc_T47601_at	T47601	3126	EST	4.05	0.00878	199.79	219.84	62.16	84.5	28.33	122.16			
rc_T53404_at	T53404	3143	EST	10.68	0.00582	654.13	475.25	687.49	48.3	0.6	93.06			
rc_T66935_at	T66935	3179	EST	3.97	0.00188	253.93	230.32	129.66	66.8	52.94	42.32			
rc_T898601_r_at	T898601	3243	EST	#N/A		839.07	747.51	231.92	410.07	342.22	200.88			
rc_T91116_at	T91116	3252	EST	4.01	0.02721	133.54	61.72	126.12	16.62	11.42	13.64			
rc_T96060_at	T96060	3263	EST	#N/A		910.76	225.75	1282.67	67.92	70.44	91.72			
			inositol 1,4,5-triphosphate receptor, type 3											
U01062_at	U01062	3273	active BCR-related gene	7.41	0	160.46	164.36	23.91	-16.8	-26.61	26.44			
U01147_at	U01147	3275	tumor necrosis factor (ligand) superfamily, member 9	3.22	0.00103	97.43	84.12	41.43	27.15	22.94	17			
U03398_at	U03398	3282	protease inhibitor 5 (maspin)	#N/A		116.17	88.07	59.5	115.08	92.7	93.14			
U04313_at	U04313	3284	cadherin 17, L1 chondroitin sulfate proteoglycan 2 (versican)	4.54	0.02986	132.77	69.67	115.99	-0.34	-2.59	9.7			
U07969_s_at	U07969	3289	intestine	10.78	0.02002	428.65	383.68	390.23	15.78	12.82	12.06			
U16306_at	U16306	3312	(versican)	#N/A		48.35	56.91	35.99	8.07	4.58	16.58			

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic: median			metastatic: median			normal set 2:		
			In metas	P value	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev	
U17760_rna1_at	U17760	3315 laminin, beta 3 (nicaein (125kD), laminin (140kD), BM600 (125kD))	3.54	0.01853	103.13	111.96	72.83	6.99	-3.15	21.08				
U20499_at	U20499	3321 sulfotransferase family 1A, phenol-prefering, member 3	5.5	0.00299	316.7	231.67	222.02	48.34	54.37	24.69				
U21049_at	U21049	3325 carcinoma, membrane associated protein 17	7.53	0.01667	202.38	248.15	119.31	-14.32	-12.21	19.43				
U38847_at	U38847	3357 TAR (HIV) RNA- binding protein 1	#N/A	#N/A	72.74	66.76	36.14	15.7	17.43	10.2				
U40990_at	U40990	3359 member 1 discoidin domain receptor family, member 1	3.18	0.00093	128.02	142.31	43.16	40.88	42.64	23.09				
U48705_rna1_s_at	U48705	3370 caudal type homeo box transcription	5.94	0.01323	178.04	200.63	102.82	-1.87	-6.25	25.81				
U51095_at U53786_at	U51095 U53786	3382 factor 1 #N/A	4.76	0.02664	130.81	143.82	93.4	5.83	5.55	8.97				
		3390 envoplakin	#N/A	#N/A	221.51	73.95	249.37	-20.54	-20.08	16.22				
U66661_at	U66661	3406 gamma-aminobutyric acid (GABA) A receptor, epsilon	#N/A	#N/A	55.33	44.93	29.26	16.58	14.81	11.96				

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change			metastatic:			metastatic:			normal		
				In metas	p value	Mean	Median	Std Dev	set 2:	Mean	Median	Std Dev	set 2:	Mean	Median
U75968_s_at	U75968	3423	(S.cerevisiae CHL1-like helicase)	#N/A	#N/A	195.48	155.37	89.8	115.5	102.24	77.72				
			O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	#N/A	#N/A	59.38	59.78	48.05	1.2	5.23	13.8				
U77413_at	U77413	3427	pyridoxal (pyridoxine, vitamin B6) kinase	3.58	0.00322	103.6	97.56	58.85	15.19	18.94	24.5				
U89606_at	U89606	3452	leukemia inhibitory factor (cholinergic differentiation factor)	#N/A	#N/A	129.58	99.52	100.52	30.69	33.06	16.14				
rc_W02695_at	W02695	3467	EphB2	9.06	0.0034	397.29	374.78	305.93	29.21	29.9	34.33				
			EST	6.23	0.01558	170.66	147.78	126.32	9.93	8.63	6.49				
			EST	31.67	0.00011	715.17	491.5	459.71	-40.13	-40.74	17.76				
rc_W46451_s_at	W46451	3529	EST	120.95	#N/A	120.95	76.95	88.42	36.63	40.09	21.06				
rc_W60968_at	W60968	3559	EST	125.7	#N/A	144.72	48.22	51.99	55.29	21.11					
rc_W67251_s_at	W67251	3570	EST	204.71	6.13	0.01463	182.17	127.82	21.77	23.88	12.17				
rc_W73189_at	W73189	3589	EST	113.63	0.02909	144.75	67.73	20.7	23.2	23.2	15.44				
rc_W78057_at	W78057	3600	EST	374.78	9.06	0.0034	397.29	305.93	29.21	29.9	34.33				
rc_W80146_f_at	W80146	3644	EST	170.66	6.23	0.01558	147.78	126.32	9.93	8.63	6.49				
rc_W92449_at	W92449	3652	EST	491.5	31.67	0.00011	715.17	459.71	-40.13	-40.74	17.76				
rc_W93726_s_at	W93726	3656	maspin	304.26	16.48	0.00014	355.41	149.69	-14.2	-14.8	10.59				
rc_W95348_at	W95348	3663	HSPC113 protein	563.86	10.89	0.01065	555.52	492.63	26.59	29.36	21.03				
rc_W95477_at	W95477	3664	EST	566.6	26.51	0.00161	941.08	1130.33	17.15	18.75	12.83				

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Affy ID	Genbank	Seq ID	Known Gene Name	In metas	p value	fold change			metastatic:			normal		
						Median	Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev	set 2: normal
X04654_s_at	X04654	3681	#N/A	98.11	89.35	38.15	42.22	41.24	17.18					17.18
X13956_at	X13956	3701	70kD polypeptide (RNP antigen) EST	3.2	0.00321	79.19	75.13	39.53	15.11	18.02	14.55			
X14850_at	X14850	3706	H2A histone family, member X	4.11	0.0001	118.41	97.53	52.6	11.6	13.26	30.46			
X16416_at	X16416	3713	v-abl Abelson murine leukemia viral oncogene homolog 1	#N/A	#N/A	82.49	90.74	16.7	36.59	38	14.59			
X54667_s_at	X54667	3731	cystatin S,cystatin SN	8.53	0.00059	273.96	169.94	217.11	-10.09	-15.68	74.88			
X57348_s_at	X57348	3744	stratifin	12.53	0.0013	308.28	241.69	194.79	-63.66	-76.43	44.95			
X57766_at	X57766	3745	stromelysin 3	#N/A	#N/A	166.25	142.96	124.34	63.38	62.13	25.48			
X63629_at	X63629	3762	cadherin 3, P-cadherin (placental)	3.02	0.01654	67.22	76.67	29.17	-4.24	-6.82	16.9			
X67325_at	X67325	3775	interferon, alpha-	9.67	0.03245	962.87	412.22	1361.55	26.81	48.73	69.77			
X76180_at	X76180	3795	inducible protein 27 sodium channel, nonvoltage-gated 1 alpha	11.68	0	320.05	268.84	127.86	22.38	23.9	15.02			
X83228_at	X83228	3810	cadherin 17, L1 cadherin (liver-intestine)	10.58	0.02147	342.12	423.87	282.49	-8.87	-6.9	8.55			
X93036_at	X93036	3830	FXYD domain-containing ion transport regulator 3	42.36	0.00167	1322.91	783.61	1219	-83.87	-85.84	40.53			

Table 9A. Genes and ESTs expressed only in metastatic liver tumor versus normal sample set 2.

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastat1			metastat1			normal set 2:		
			In metas	p value	c: Mean	c: Median	c: Std Dev	c: Mean	c: Std Dev	Median	Std Dev	normal	set 2:	normal
rc_AA001902_at	AA001902	5 KIAA0305 gene product	#N/A	#N/A	14.88	17.06	8.8	29.11	28.6	23.36	23.36	23.36	23.36	
rc_AA001903_1_at	AA001903	6 EST	#N/A	#N/A	6.64	0.97	14.07	26.52	28.7	13.21	13.21	13.21	13.21	
rc_AA004669_at	AA004669	9 EST	#N/A	#N/A	8.66	10.77	8.65	33.32	25.36	31.12	31.12	31.12	31.12	
rc_AA004707_at	AA004707	10 copper chaperone for superoxide dismutase	#N/A	#N/A	217.76	217.72	144.41	502.14	479.38	161.01	161.01	161.01	161.01	
rc_AA005202_at	AA005202	12 retinol-binding protein 4, interstitial	3.18	0.00106	43.46	41.24	9.66	163.36	107.5	110.2	110.2	110.2	110.2	110.2
rc_AA009719_at	AA009719	20 peroxisomal membrane protein 2 (22kD)	47.12	0.00008	-50.14	-51.69	47.17	1370.32	1503.99	715.62	715.62	715.62	715.62	715.62
rc_AA010205_at	AA010205	23 EST	7.41	0	14.43	17.64	14.87	187.55	154.99	92.13	92.13	92.13	92.13	92.13
rc_AA010360_at	AA010360	24 EST	6.55	0.00027	12.5	14.77	8.62	169.99	135.98	129.2	129.2	129.2	129.2	129.2
rc_AA010619_at	AA010619	27 EST	8.55	0.00057	21.58	5.47	42.99	278.66	268.6	154.98	154.98	154.98	154.98	154.98
rc_AA013095_s_at	AA013095	33 potassium voltage-gated channel, shaker-related subfamily, beta member 1, EST	#N/A	#N/A	7.81	3.06	19.71	18.56	15.83	8.24	8.24	8.24	8.24	8.24
rc_AA015768_at	AA015768	34 ubiquitin-like 3	15.3	0.00008	12.22	14.2	11.71	417.95	472.1	248.15	248.15	248.15	248.15	248.15
rc_AA016021_at	AA016021	35 AA017146_at	#N/A	#N/A	13.88	16.21	13.21	65.65	51.44	46.44	46.44	46.44	46.44	46.44
rc_AA017146_at	AA017146	36 AA018867_at	10.1	0.00052	30.35	22.85	50.05	414.24	435.09	193.39	193.39	193.39	193.39	193.39
rc_AA018867_at	AA018867	39 AA019715_at	42.87	0.00002	45.29	29.28	52.68	1944.56	2160.33	1142.41	1142.41	1142.41	1142.41	1142.41
rc_AA019715_at	AA019715	41 EST	#N/A	#N/A	8.03	8.03	6.49	15.9	14.58	7.82	7.82	7.82	7.82	7.82
rc_AA024511_at	AA024511	46 suppressor of Ty (S.cerevisiae) 3 homolog	#N/A	#N/A	7.82	3.08	12.06	62.54	58.34	27.73	27.73	27.73	27.73	27.73
rc_AA024866_at	AA024866	49 EST	#N/A	#N/A	10.89	7.87	8.56	31.16	30.56	14.26	14.26	14.26	14.26	14.26

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastati			normal			normal		
			In metas	p value	c: Mean	c: Std Dev	metastati	c: Mean	c: Std Dev	metastati	c: Mean	c: Std Dev	set 2: Median	set 2: Std Dev
rc_AA025930_at	AA025930	52 EST	3.59	0.00372	33.24	25.62	26.11	115.2	110.13	45.17				
microvascular endothelial differentiation gene 1														
AA027766_at	AA027766	58	EST	#N/A	16.71	7.36	25.05	26.19	13.26					
AA028976_at	AA028976	63	EST	#N/A	9.46	10.28	18.91	72.06	47.28	55.89				
rc_AA031360_s_at	AA031360	67	EST	#N/A	13.46	12.87	10.49	26.25	24.36	9.3				
rc_AA032250_at	AA032250	73	EST	3.56	0.0009	10.56	13.86	9.55	84.44	83.69	50.06			
rc_AA034365_at	AA034365	76	EST	#N/A	119.56	39.46	171.27	216.28	159.86	152.39				
rc_AA039616_at	AA039616	90	EST	9.36	0.00009	2.48	-4.83	14.2	238.71	224.42	125.28			
rc_AA040087_at	AA040087	92	EST	4.13	0.00123	34.99	27.32	18.99	156.63	148.88	90.44			
rc_AA040291_at	AA040291	94	KIAA0669 gene product	3.55	0.00308	12.98	12.72	16.36	101.69	98.94	80.43			
NADH dehydrogenase (ubiquinone) 1 beta														
AA041208_at	AA041208	96	subcomplex, 8 (19kD, ASHI)	#N/A	234.76	302.34	215.51	448.34	390	234.61				
rc_AA043790_at	AA043790	99	KIAA0937 protein	#N/A	5.63	7.44	12.94	32.16	31.34	10.66				
AA044095_at	AA044095	102	EST	#N/A	29.41	18.4	35.04	31.85	24.92	38.98				
AA044842_at	AA044842	105	Autosomal Highly Conserved Protein	5.21	0.0009	16.66	16.52	18	167.15	159.32	123.77			
rc_AA045481_at	AA045481	107	EST	#N/A	28.81	21.88	17.14	71.32	63.94	38.49				
rc_AA046457_at	AA046457	111	EST	3.2	0.00513	77.66	80.71	27.66	304.54	264.9	233.62			
rc_AA046747_at	AA046747	114	EST	4.82	0.00022	-5.19	-4.2	10.73	113.78	88.54	68.41			
AA047151_at	AA047151	116	EST	7.13	0.00007	17.55	17.5	10.09	188.62	185.41	80.5			
rc_AA053917_at	AA053917	131	EST	#N/A	-18.24	-11.6	21.61	56.08	38.68	82.71				
rc_AA055992_at	AA055992	136	calumenin	3.51	0.00604	80.45	65.8	47.34	276.06	265.13	141.34			
AA056319_at	AA056319	139	EST	#N/A	21.89	17.62	12.89	29.23	26.53	11.96				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			normal			normal		
			In metas	p value	c: Std Dev	c: Std Dev	set 2: Median	set 2: Mean	set 2: Median	set 2: Mean	Std Dev	Std Dev	Std Dev	Std Dev
rc_AA056482_at	AA056482	141 EST	4.82	0.00199	10.09	19.17	14.96	135.83	132.94	97.88				
SEC24 (S. cerevisiae)														
rc_AA056735_at	AA056735	142 D	#N/A	#N/A	4.59	10.03	14.42	29.84	28.43	10.97				
rc_AA074885_at	AA074885	161 EST	11.05	0.00786	79.55	25.58	153.64	652.03	761.74	300.57				
rc_AA075298_at	AA075298	163 EST	#N/A	#N/A	46.45	36.93	42.61	129.13	121.57	70.36				
rc_AA076672_at	AA076672	172 EST	#N/A	#N/A	86.18	87.53	60.88	122.82	105.84	54.8				
rc_AA084286_at	AA084286	176 EST	#N/A	#N/A	-2.06	0.32	14.88	30.7	26.84	20.69				
rc_AA084318_at	AA084318	177 EST	#N/A	#N/A	9.73	3.97	17.06	30.63	32.37	11.48				
rc_AA086201_at	AA086201	185 EST	5.8	0.00012	21.29	24.75	14.37	177.39	182.95	95.51				
AA092376_at	AA092376	196 15 kDa selenoprotein	#N/A	#N/A	16.78	14.2	28.1	59.07	57.94	24.97				
AA092596_at	AA092596	197 6 HLA-B associated transcript-	3.46	0.02532	30.18	22.69	61.67	148.47	171.15	77.57				
AA092716_at	AA092716	198 3	13.97	0.00009	62.83	63.53	42.33	952.09	817.41	545.31				
rc_AA098864_at	AA098864	205 EST	#N/A	#N/A	30.42	31.06	18.38	56.43	52.57	21.3				
rc_AA099225_at	AA099225	206 EST	7.33	0.00062	4.37	1.35	6.08	212.68	163.45	194.31				
rc_AA099571_at	AA099571	209 MD-2 protein	#N/A	#N/A	10.12	4.61	19.11	55.77	62.72	31.71				
rc_AA102098_at	AA102098	218 EST	#N/A	#N/A	-1.8	-5.18	15.21	21.79	20.01	6.78				
rc_AA102571_at	AA102571	220 EST	#N/A	#N/A	8.7	12.32	15.12	17.15	15.33	7.6				
rc_AA112209_s_at	AA112209	223 acyl-Coenzyme A dehydrogenase, long chain	3.37	0.00084	29.77	28.31	11.33	116	100.18	66.07				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in metas		metastati c:		metastati c: Std Dev		normal set 2: Median		normal set 2: Std Dev	
			in metas	P value	Mean	Median	Mean	Median	Mean	Median	Mean	Median
rc_AA115933_s_at	AA115933	KIAA1098 protein	#N/A	#N/A	8.62	6.46	10.77	33.88	34.38	34.38	16.63	16.63
rc_AA116075_at	AA116075	EST	#N/A	#N/A	29.71	23.88	10	62.94	64.79	64.79	25.13	25.13
rc_AA121140_at	AA121140	EST	3.33	0.00058	6.67	5.82	3.73	74.84	83.56	83.56	31.9	31.9
rc_AA121257_at	AA121257	EST	#N/A	#N/A	21.76	21.21	32.49	42.39	43.62	43.62	11.55	11.55
rc_AA126059_at	AA126059	EST	3.08	0.00706	102.34	104.33	40.8	380.92	280.71	280.71	316.4	316.4
rc_AA127514_at	AA127514	EST	3.4	0.00045	11.36	10.76	6.8	74.71	76.5	76.5	36.07	36.07
rc_AA127646_at	AA127646	protein 1	#N/A	#N/A	6.76	-0.26	12.36	44.24	41.48	41.48	20.02	20.02
rc_AA128177_at	AA128177	sequence-specific single-stranded-DNA-binding protein	#N/A	#N/A	11.71	6.05	16.96	44.4	33.57	33.57	33.54	33.54
rc_AA129465_f_at	AA129465	EST	#N/A	#N/A	7.9	10.16	24.29	61.62	59.75	59.75	34.37	34.37
rc_AA133214_s_at	AA133214	meningioma expressed antigen 6 (coiled-coil proline-rich) calcitonin receptor-like receptor activity modifying protein 1	#N/A	#N/A	3.16	7.46	14.35	65.17	56.11	56.11	51.18	51.18
rc_AA133215_at	AA133215	protein 1	4.55	0.02092	76.1	37.86	72.97	250.94	266.82	266.82	64.2	64.2
rc_AA133457_at	AA133457	EST	#N/A	#N/A	233.92	279.32	161.44	456.09	475.45	475.45	114	114
rc_AA136333_at	AA136333	zinc finger protein	#N/A	#N/A	17.23	17.21	5.7	45.55	39.88	39.88	25.1	25.1
rc_AA136611_at	AA136611	EST	#N/A	#N/A	9.05	6.82	8.39	48.23	42.67	42.67	13.53	13.53
rc_AA136940_at	AA136940	EST	#N/A	#N/A	40.81	41.78	20.7	79.13	73.37	73.37	41.89	41.89
AA143019_at	AA143019	EST	6.75	0.00109	-0.4	-5.82	18.62	192.42	176.13	176.13	136.81	136.81
rc_AA147626_at	AA147626	EST	#N/A	#N/A	37.93	20.43	44.09	82.38	75.98	75.98	37.45	37.45
rc_aa147646_s_at	AA147646	DKFZP586A0522 protein	21.82	0	15.59	14.85	24.51	610.52	685.45	685.45	288.9	288.9
rc_AA148480_s_at	AA148480	flavin containing monooxygenase 5	19.64	0	18.26	14.26	14.85	521.95	407.11	407.11	247.99	247.99

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			normal			normal		
			In metas	p value	c: Mean	c: Median	c: Std Dev	set 2: Median	set 2: Mean	set 2: Std Dev	set 2: Median	set 2: Mean	set 2: Std Dev	
rc_AA148539_at	AA148539	319 EST	#N/A	9.96	9.87	8.65	28.88	25.89	6.73					
rc_AA149253_at	AA149253	323 EST	5.12	0.00863	78.65	75.3	61.14	401.77	301.06	333.03				
rc_AA150205_at	AA150205	328 EST	#N/A	#N/A	-1.1	-1.72	9.15	8.12	7.44	9.59				
rc_AA150284_at	AA150284	329 EST	#N/A	#N/A	28.51	25.35	17.97	41.67	43.94	18.29				
rc_AA151243_at	AA151243	334 EST	#N/A	#N/A	1.13	-0.17	14.55	43.61	42.74	11.08				
S-adenosylhomocysteine hydrolase-like 1														
AA157401_at	AA157401	346	#N/A	15.44	13.27	14.06	61.17	65.58	27.48					
rc_AA167550_at	AA167550	361 EST	#N/A	4.38	7.64	6.98	28.69	26.29	16.06					
rc_AA171529_at	AA171529	365 EST	#N/A	#N/A	-1.76	-4.58	6.37	51.3	47.89	33.98				
AA174202_at	AA174202	375 EST	#N/A	#N/A	55.99	38.87	72.55	120.99	128.88	62.33				
rc_AA179004_at	AA179004	377 EST	14.34	0.00008	-33.2	-28.97	78.62	503.76	495.87	326.16				
rc_AA182030_at	AA182030	387 EST	8.32	0.00018	14.05	16.82	12.13	222.23	220.01	117.56				
STAT induced STAT inhibitor-2														
rc_AA182568_at	AA182568	388 EST	10.92	0.00099	23.5	18.15	21.15	501.87	386.2	478.02				
rc_AA187437_at	AA187437	389 EST	#N/A	#N/A	33.59	47.3	26.91	62.23	63	25.01				
protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform														
rc_AA191310_s_at	AA191310	397	0	26.23	29.87	6.93	206.65	209.15	77.34					
rc_AA193671_at	AA193671	405 KIAA0580 protein	#N/A	40.18	43.2	23.51	64.83	38.29	71.28					
eukaryotic translation initiation factor 4A, isoform 2														
AA195179_s_at	AA195179	415	#N/A	30.71	38.24	25.48	85.7	87.87	42.11					
rc_AA195463_at	AA195463	416 EST	#N/A	#N/A	5.44	6.92	3.77	51.81	64.76	26.85				
rc_AA195515_at	AA195515	417 EST	#N/A	#N/A	7.27	3.56	8.61	51.59	49.91	23.13				
rc_AA195657_at	AA195657	419 EST	6.44	0.00016	5.72	7.44	9.74	157.7	136.21	100.68				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			metastatic			normal		
			In metas	p value	c: Median	c: Mean	c: Std Dev	c: Median	c: Mean	c: Std Dev	set 2: Median	set 2: Mean	set 2: Std Dev	
Intercellular adhesion														
rc_AA197311_s_at	AA197311	molecule 1 (CD54), human	6.07	0.00053	-19.49	1.63	43.72	154.69	175.76	83.19				
rc_AA199603_at	AA199603	rhinovirus receptor	#N/A	#N/A	14.97	24.27	28.57	54.95	55.7	19.61				
rc_AA211370_at	AA211370	EST	#N/A	#N/A	27.26	29.44	16.5	44.85	45.87	21.25				
rc_AA211418_at	AA211418	EST	#N/A	#N/A	65.81	70.1	37.84	223.56	214.42	151.4				
rc_AA223902_at	AA223902	EST	9.91	0.00003	7.98	-3.32	28.42	292.86	294.78	156.98				
rc_AA226925_at	AA226925	EST	#N/A	#N/A	11.94	9.22	7.55	49.69	48.29	27.49				
rc_AA227480_s_at	AA227480	pim-2 oncogene	3.31	0.02413	48	62.07	33.49	195.79	162.34	182.76				
rc_AA227968_at	AA227968	histone deacetylase 6	#N/A	#N/A	177.49	137.57	94.86	349.29	340.4	101.81				
rc_AA232114_s_at	AA232114	epoxide hydrolase 2, cytoplasmic	24.34	0.00007	63.09	46.66	60.38	1455.28	1626.11	664.36				
rc_AA233126_at	AA233126	EST	#N/A	#N/A	48.86	59.64	33.59	88.56	74.17	35.35				
rc_AA233152_at	AA233152	EST	12.95	0	-29.09	-28.01	34.42	299.54	291.48	156.26				
rc_AA233225_at	AA233225	MRS1 protein	#N/A	#N/A	25.16	30.66	26.03	54.1	55.8	22.69				
rc_AA233369_at	AA233369	histidine ammonia-lyase	9.06	0.00008	49.39	47.92	39.8	425.35	405.81	214.85				
rc_AA233763_at	AA233763	EST	4.61	0.00004	25.29	36.26	17.49	146.52	139.66	60.53				
rc_AA233797_at	AA233797	sperm associated antigen 7	#N/A	#N/A	54.72	50.23	11.36	116.14	127.3	54.24				
rc_AA233837_at	AA233837	EST	4.79	0.0034	18.96	19.45	40.67	214.77	118.28	278.62				
CCAAT/enhancer binding														
AA234634_f_at	AA234634	protein (C/EBP), delta	7.48	0.03318	158.16	49.12	223.12	621.92	588.94	332.64				
AA234687_at	AA234687	EST	#N/A	#N/A	-8.8	-12.38	20.12	61.87	47.79	57.62				
rc_AA234717_at	AA234717	EST	#N/A	#N/A	10.99	5.01	20.04	50.22	53.32	31.32				
AA234817_at	AA234817	EST	6.22	0.00099	31.51	20.97	34.92	222.41	156.99	133.06				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			normal			normal		
			In metas	p value	c: Mean	Median	c: Std Dev	Mean	Median	c: Std Dev	Mean	Median	c: Std Dev	
rc_AA234831_at	AA234831	491 EST	3.42	0.00206	23.54	21.62	28.81	112.19	119	49.23				
rc_AA235288_at	AA235288	494 1 PTP1-associated RhoGAP	3.7	0.00643	34.06	30.95	14.36	169.9	113.81	138.05				
rc_AA235507_at	AA235507	498 subfamily a, 5	3.28	0.00249	22.14	37.31	26.61	111.91	126.75	58.39				
rc_AA242822_at	AA242822	524 EST	#N/A	#N/A	9.44	13.66	8.25	27.21	25.96	16.64				
rc_AA243654_at	AA243654	532 EST	#N/A	#N/A	0.67	3.93	11.08	69.19	62.85	48.63				
rc_AA247453_at	AA247453	533 EST	3.09	0.0015	32.38	37.86	21.04	120.43	133.44	58.12				
rc_AA250958_f_at	AA250958	538 EST	#N/A	#N/A	53.41	53.63	22.55	99.74	114.71	55.23				
rc_AA251114_at	AA251114	539 overexpressed gene 1	6.6	0.00039	28.47	18.55	28.89	219.81	202.99	87.55				
rc_AA251776_at	AA251776	545 Jun D proto-oncogene	#N/A	#N/A	30.8	23.59	32.23	51.25	46.83	15.96				
rc_AA251845_at	AA251845	548 EST	#N/A	#N/A	269.35	283.55	60.62	477.47	411.47	377.99				
rc_AA253410_at	AA253410	564 EST	#N/A	#N/A	18.46	7.23	42.79	49.37	26.82	45.2				
rc_AA255546_at	AA255546	569 EST	4	0.00301	61.04	67.88	31.64	260.34	224.12	142.84				
rc_AA255903_at	AA255903	573 CD39-like 4	5.67	0.01687	72.5	39.23	108.82	383.56	374.1	211.92				
rc_AA256341_at	AA256341	578 EST	7.37	0.00091	17.81	2.34	28.59	280.57	324.08	170.98				
rc_AA256990_at	AA256990	585 EST	#N/A	#N/A	8.43	11.36	27.79	15.63	16.56	6.89				
rc_AA257057_s_at	AA257057	586 EST	8.11	0.00379	42.36	16.78	47.02	451.86	462.6	343.05				
rc_AA258158_at	AA258158	588 EST	#N/A	#N/A	7.91	2.43	17.94	44.84	34.32	35.63				
rc_AA258353_at	AA258353	593 EST	5.28	0.00193	71.76	84	37.77	347.7	363.14	106.2				
rc_AA259064_at	AA259064	602 EST	13.15	0.00001	15.32	-1.37	28.67	401.93	394.99	178.23				
rc_AA278670_at	AA278670	616 EST	#N/A	#N/A	7.44	11.47	12.63	54.24	49.98	28.69				
rc_AA278824_at	AA278824	619 EST	#N/A	#N/A	26.85	31.59	11.72	83.48	91.25	30.24				
rc_AA278853_at	AA278853	621 EST	#N/A	#N/A	10.28	11.7	21.49	42.68	43.68	17.64				
rc_AA279158_1_at	AA279158	623 EST	#N/A	#N/A	50	46.97	19.41	87.9	72.44	38.36				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change	In metas	p value	c: Mean	c: Median	c: Std Dev	normal		normal		normal	
										#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
rc_AA279341_at	AA279341	625	EST				67.56	80.37	50.19	132.89	118.11	67.28			
rc_AA279916_at	AA279916	633	EST				61.08	56.18	25.7	115.24	102.89	58.77			
spleen focus forming virus (SFFV) proviral Integration oncogene sp1				4.46	0.02062	64.05	69.15	51.55	339.15	353.53	235.59				
rc_AA280413_s_at	AA280413	638	EST		0.00002	6.52	-0.81	16.89	87.27	85.27	34.29				
rc_AA281545_at	AA281545	645	EST												
seven in absentia (Drosophila) homolog 1 mannose-P-dolichol utilization defect 1				3.96	0.00094	7.67	4.72	15.41	103.75	79.4	70.74				
rc_AA281770_at	AA281770	649	EST				3.3	0.04108	65.08	53.58	57.86	170.88	165.02	41.87	
rc_AA281796_at	AA281796	650	EST				#N/A	#N/A	7.18	5.97	14.25	31.31	28.9	13.53	
rc_AA282541_at	AA282541	661	EST				#N/A	#N/A	0.28	-9.07	30.81	59.89	51.54	35.5	
rc_AA282956_at	AA282956	664	EST				#N/A	#N/A	21.18	25.64	13.39	67.44	59.46	35.89	
rc_AA283066_at	AA283066	666	EST												
phosphatidylethanolamine N-methyltransferase				10.03	0.00019	44.8	62.07	44.12	514.93	591.52	206.4				
rc_AA284795_at	AA284795	678	EST		6.95	0.00125	12.65	14.54	23.53	238.16	242.27				
rc_AA285053_at	AA285053	681	EST												
rc_AA286710_at	AA286710	683	lymphocyte adaptor protein		#N/A	#N/A	37.88	39.15	30.32	82.93	86.15	45.58			
rc_AA287566_at	AA287566	690	KIAA0187 gene product		9.07	0.00013	4.86	6.24	7.4	246.24	201.66	228.64			
rc_AA291293_at	AA291293	698	EST		#N/A	#N/A	17.35	18.07	17.24	33.6	33.3	5.56			
AA292440_s_at	AA292440	709	DKFZP566B133 protein		#N/A	#N/A	122.1	125.27	37.73	370.32	318.31	181.37			
AA296821_at	AA296821	723	EST		#N/A	#N/A	15.47	10.65	21.91	57.72	71.28	33.61			
AA298180_at	AA298180	726	EST		3.11	0.00747	19.6	25.9	18.83	109.91	84.28	88.07			
rc_AA312946_s_at	AA312946	731	EST		9.21	0.00106	12.32	13.78	12.24	300.22	304.56	213.18			

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastati c:			normal set 2:			normal set 2:		
			in metas	p value	c: Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev	
fatty-acid-Coenzyme A ligase, long-chain 3														
AA316272_at	AA316272	734	#N/A	34.62	38.08	17.08	71.9	73.01	27.47					
AA328694_at	AA328694	737	EST	#N/A	49.88	48.15	31.41	115.97	114.66	46.25				
rc_AA342918_at	AA342918	750	EST	#N/A	23.67	31.68	25.77	69.4	73.71	18.13				
rc_AA343142_at	AA343142	751	EST	20.87	0.00003	-12.34	-21.46	30.45	610.64	636.83	438.33			
complement component 8, gamma polypeptide														
rc_AA344866_s_at	AA344866	752	EST	7.28	0.00206	292.65	305.28	176.61	1845.16	1679.29	561.04			
rc_AA363203_s_at	AA363203	761	EST	#N/A	35.7	40.27	34.51	78.45	75.11	47.8				
rc_AA365691_at	AA365691	763	EST	#N/A	48.01	47.17	25.37	28.69	26.73	13.89				
rc_AA381125_at	AA381125	772	EST	15.48	0	17.66	13.82	13.2	412.26	344.45	217.56			
AA397841_at	AA397841	780	EST	8.21	0	7.72	3.33	18.47	214.17	189.93	116.41			
rc_AA397904_at	AA397904	781	EST	#N/A	22.74	18.55	19.05	59.75	54.83	32.24				
rc_AA397919_at	AA397919	785	EST	#N/A	108.63	144.35	84.25	243.79	188.62	185.4				
growth factor receptor-bound protein 14														
rc_AA398124_s_at	AA398124	787	EST	7.82	0.00009	3.4	5.86	7.61	189.27	167.23	110.44			
rc_AA398280_at	AA398280	792	EST	12.43	0.00134	-114.74	-71.05	103.33	433.45	423.73	356.61			
rc_AA398386_at	AA398386	793	EST	5.71	0.00007	10.59	16.25	21.59	153.16	164.38	83.94			
rc_AA398423_at	AA398423	795	EST	8.26	0.00063	-17.3	-16.19	23.92	230.91	250.5	156.29			
rc_AA398674_at	AA398674	798	thrombospondin 1	#N/A	-27.87	14.49	146.65	137.87	96.14					
rc_AA400030_at	AA400030	806	EST	3.98	0.00088	8.99	12.21	11.35	97.83	115.15	52.04			
rc_AA400080_at	AA400080	807	EST	#N/A	25.33	23.57	27.54	61.21	60.21	29.91				
rc_AA400258_at	AA400258	812	EST	11.89	0.00478	85.31	36.81	139.93	827.48	884.35	562.14			

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			metastatic			normal		
			In metas	p value	c: Std	c: Mean	Median	Dev	c: Std	Mean	Median	Dev	set 2: Std Dev	set 2: Std Dev
tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntington interacting protein L; transcription factor IIIA-interacting protein														
AA400333_at	AA400333	815			#N/A	27.22	27.33	24.37	62.54	58.6	31.69			
rc_AA400934_at	AA400934	824	EST		4.98	0.02013	75.44	67.21	77.7	305.09	307.45	125.76		
rc_AA400979_at	AA400979	825			6.65	0.01051	48.89	21.04	80.4	276.38	267.3	88.7		
rc_AA401091_at	AA401091	826	EST		#N/A	#N/A	31.88	32.59	43.51	30.55	19.82	28.68		
rc_AA401562_s_at	AA401562	830	EST		50.45	0.00301	155.46	63.87	317.6	3745.71	3628.4	1635.98		
rc_AA401825_at	AA401825	831	EST		#N/A	#N/A	24.3	26.82	18.04	65.22	57.51	46.54		
rc_AA402224_at	AA402224	836			14.41	0.00012	37.55	48.88	48.58	749.36	812.2	443.66		
rc_AA402610_at	AA402610	839	KIAA0548 protein		#N/A	#N/A	3.02	6.69	13.83	27.54	23.2	17.78		
rc_AA402656_at	AA402656	841	EST		12.05	0.00001	-2.56	18.8	40.57	342.11	315.47	205.61		
AA404214_at	AA404214	846	EST		#N/A	#N/A	35.28	48.54	23.52	70.66	66.71	55.97		
rc_AA404248_at	AA404248	847	EST		#N/A	#N/A	11.96	11.18	10.84	40.92	35.06	17.49		
rc_AA404352_at	AA404352	850	EST		7	0.00059	26.7	20.02	33.28	213.01	172.11	108		
rc_AA405494_at	AA405494	858	EST		#N/A	#N/A	10.03	9.53	7.62	59.95	44.88	50.8		
rc_AA405495_at	AA405495	859	EST		#N/A	#N/A	26.12	22.63	43.42	79	82.8	30.16		
rc_AA405744_at	AA405744	863	EST		#N/A	#N/A	61.18	28.74	58.71	64.39	57.95	35.67		
rc_AA406363_at	AA406363	874	EST		#N/A	#N/A	6.85	5.69	15.69	35.62	35.06	13.69		

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change		metastati c:		metastati c: Std Dev		normal set 2: Median		normal set 2: Std Dev	
			in metas	p value	Median	Mean	Median	Mean	Median	Mean	Median	Mean
rc_AA406546_at	AA406546	EST	#N/A	#N/A	-1.45	-7.89	15.19	46.62	50.65	26.97		
rc_AA406610_at	AA406610	EST	#N/A	#N/A	5.99	6.04	4.63	35.94	34.84	11.57		
rc_AA410255_at	AA410255	EST	7.56	0.00043	0.82	4.15	11.49	195.75	236.93	110.49		
rc_AA411795_at	AA411795	EST	#N/A	#N/A	72.18	53.17	44.28	130.27	131.65	23.71		
rc_AA412063_at	AA412063	EST	8.26	0.00001	11.36	14.03	19.55	220.12	187.85	149.43		
rc_AA412068_at	AA412068	EST	#N/A	#N/A	30.52	29.79	13.4	81.26	74.52	35.68		
rc_AA412149_at	AA412149	KIAA0480 gene product	#N/A	#N/A	14.07	10.08	14.16	37.43	32.4	15.56		
rc_AA412520_at	AA412520	EST	#N/A	#N/A	18.84	14.4	14.11	80.29	103.19	41.98		
rc_AA412700_at	AA412700	ubiquitin-conjugating enzyme E2L 6	#N/A	#N/A	139.65	95.44	135.61	275.39	273.98	112.87		
5-methyltetrahydrofolate-homocysteine methyltransferase reductase												
rc_AA416936_at	AA416936	910	EST	4.98	0.00632	82.04	85.81	69.18	427.41	366.53	235.63	
rc_AA417078_at	AA417078	916	EST	4.1	0.00414	36.75	35.35	15.12	189.88	171.1	150.02	
rc_AA418398_at	AA418398	921	EST	#N/A	#N/A	0.1	-6.02	17.92	30.41	32	20.72	
rc_AA419608_at	AA419608	925	EST	9.19	0.00005	51.89	51.37	25.93	524.34	571.05	296.46	
rc_AA419622_at	AA419622	926	EST	4.62	0.00386	24.88	17.15	26	158.88	162.5	112.57	
rc_AA421051_at	AA421051	928	serum-inducible kinase	#N/A	#N/A	42.94	7.14	87.89	51.27	.. 45.65	28	
branched chain alpha-ketoacid dehydrogenase kinase												
rc_AA421052_at	AA421052	929	kinase	3.52	0.00869	77.76	94.75	43.63	251.45	221.35	109.93	
rc_AA421561_at	AA421561	933	Insulin-like growth factor 2 (somatomedin A)	9.98	0.00007	79.46	77.34	41.63	921.91	703.16	679.72	

Table 9B: Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	in metas	P value	metastati		metastati		normal	
					fold change	c: Median	c: Std Dev	set 2: Median	set 2: Std Dev	
AA424307_at	AA424307	944 EST	5.73	0.0074	44.98	21.05	54.01	202.82	194.92	68.07
rc_AA424798_at	AA424798	947 EST	17.45	0.00352	48.63	15.48	171.26	879.91	873.25	489.59
rc_AA425214_at	AA425214	950 EST	#N/A	#N/A	2.71	2.07	4.88	21.4	20.31	10.15
rc_AA426643_at	AA426643	970 EST	#N/A	#N/A	9.96	0.97	18.11	48.26	47.37	23.47
rc_AA427537_at	AA427537	974 DKFZP566J153 protein regulator of G-protein signalling 14	#N/A	#N/A	183.26	156.56	68.58	259.57	242.97	79.81
rc_AA427579_at	AA427579	975 midline 2	#N/A	#N/A	13.35	13.28	16.49	34.79	25.25	25.11
rc_AA427819_at	AA427819	980 EST	3.44	0.00063	25.98	17.06	14.91	97.03	93.49	31.39
rc_AA428150_at	AA428150	985 EST	5.24	0.00167	41.92	35.06	30.53	213.96	217.27	76.08
rc_AA428325_at	AA428325	988 EST	8.36	0.00002	-0.52	3.28	16.92	194.02	167.37	111.11
rc_AA428900_at	AA428900	992 EST	7.01	0.00037	66.25	66.77	15.35	619.96	619.42	441.72
rc_AA429038_at	AA429038	995 EST	3.29	0.00927	13.39	1.93	28.01	108.66	87.59	86.11
rc_AA429478_at	AA429478	998 EST	3.41	0.02599	55.86	65.19	47.48	192.7	196	89.2
rc_AA429651_at	AA429651	1002 KIAA0871 protein	#N/A	#N/A	15.52	13.25	17.03	44.75	41.91	28.67
succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD										
rc_AA432166_f_at	AA432166	1030 serum constituent protein	#N/A	#N/A	10.94	14.1	42.99	33.86	42.75	27.46
rc_AA434225_at	AA434225	1035 kinesin family member 3B	#N/A	#N/A	1010.84	876.42	674.94	1022.5	746.49	681.49
rc_AA435591_at	AA435591	1038 AA435753	3.5	0.0001	3.57	3.68	10.34	75.9	81.12	29.32
rc_AA435753_at	AA435753	1045 EST	4.71	0.00078	198.97	193.33	110.58	970.79	830.39	567.79
rc_AA436156_s_at	AA436156	1051 EST	#N/A	#N/A	22.66	7.78	34.68	54.98	48.35	38.09
rc_AA436548_at	AA436548	1054 EST	#N/A	#N/A	5.08	5.93	5.2	40.27	38.99	22.22
rc_AA436880_at	AA436880	1058 EST	3.22	0.00699	4.71	9.21	13.85	86.89	68.41	66.5

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic c: Std Dev			normal set 2: Mean			normal set 2: Median			normal set 2: Std Dev		
			In metas	p value	c: Mean	c: Std Dev	metastatic c: Mean	metastatic c: Std Dev	normal set 2: Mean	normal set 2: Median	normal set 2: Std Dev	normal set 2: Mean	normal set 2: Median	normal set 2: Std Dev	normal set 2: Mean	normal set 2: Median	normal set 2: Std Dev
rc_AA437295_at	AA437295	1062 ribosomal protein L7a transmembrane 7	4.35	0.00347	19.67	20.38	43.07	139.16	140.38	140.38	70.9						
rc_AA443658_at	AA443658	1079 superfamily member 2	9.06	0.00048	4.48	17.91	24.51	276.02	194.73	194.73	227.48						
rc_AA443934_at	AA443934	1083 GTP-binding protein Rho7	3.09	0.00214	30.32	35.97	13.76	115.87	113.7	113.7	66.78						
rc_AA446342_at	AA446342	1088 (Drosophila) homolog 1	4.84	0.00015	9.92	9.12	4.58	110.73	115.89	115.89	53.13						
rc_AA447802_at	AA447802	1108 EST	#N/A	#N/A	15.64	17.7	13.81	21.51	21.34	21.34	7.37						
rc_AA447876_at	AA447876	1109 EST	#N/A	#N/A	13.05	6.78	34.07	27.08	22.86	22.86	22.46						
FXYD domain-containing ion transport regulator 1																	
rc_AA448300_at	AA448300	1116 (phospholemman)	24.97	0.00001	118.64	81.63	70.34	2849.54	2905.51	2905.51	994.41						
rc_AA449108_at	AA449108	1118 EST	#N/A	#N/A	10.9	18.13	15.28	52.58	57.3	57.3	23.76						
rc_AA449297_at	AA449297	1121 EST	3.78	0.00039	3.76	0.63	19.01	91.67	81.15	81.15	55.17						
rc_AA452158_at	AA452158	1141 member B	28.96	0.00064	-103.87	-106.99	71.68	1071.9	1164.8	1164.8	789.64						
rc_AA453770_s_at	AA453770	1157 EST	6.04	0.00524	46.33	25.95	53.45	217.46	212.4	212.4	70.02						
rc_AA454177_l_at	AA454177	1164 EST	10.3	0.0008	9.16	14.72	11.39	324.16	253.23	253.23	258.82						
rc_AA454667_at	AA454667	1167 EST	#N/A	#N/A	21.25	12.77	23.4	83.02	75.81	75.81	56.63						
rc_AA455111_at	AA455111	1173 ribonucleoprotein C (C1/C2)	#N/A	#N/A	-31.71	-40.39	38.45	38.96	36.83	36.83	26.21						
rc_AA455261_at	AA455261	1175 chromobox homolog 7	#N/A	#N/A	32.5	45.54	26.51	66.78	66.08	66.08	30.15						

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change			metastati c:			normal set 2: Mean			normal set 2: Std Dev		
				In metas	p value	metastati c: Mean	Median	c: Std Dev	metastati c: Mean	Median	c: Std Dev	metastati c: Mean	Median	c: Std Dev	
rc_AA455865_at	AA455865	1180	phosphatidylinositol glycan, class B	5.41	0.00004	11.68	8.67	10.65	133.15	134.74	63.3				
rc_AA455896_s_at	AA455896	1181	glypican 1	3.46	0.00887	16.1	4.35	40.39	120.52	137.84	66.93				
rc_AA455987_at	AA455987	1183	EST	5.36	0.00029	20.54	17.51	15.24	128.55	130.64	17.07				
butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase)															
rc_AA455988_at	AA455988	1184	RAD23 (S. cerevisiae)	15.54	0.00001	10.13	11.88	8.38	354.42	375.91	141.08				
rc_AA456075_at	AA456075	1186	homolog A	#N/A	#N/A	33.34	38.35	32.93	90.47	66.92	66.03				
rc_AA456080_at	AA456080	1187	EST	#N/A	#N/A	32.35	17.59	33.21	27.76	26.18	12.38				
rc_AA456147_at	AA456147	1188	III A	4.23	0.00088	4.61	0.17	9.08	102.1	89.95	63.84				
rc_AA456289_at	AA456289	1189	EST	15.31	0.00004	18.07	17.84	39.22	512.64	542.52	303.15				
rc_AA456326_at	AA456326	1191	EST	3.35	0.00489	17.08	2.74	30.38	111.5	102.17	68.09				
rc_AA456612_at	AA456612	1195	EST	#N/A	#N/A	164.11	136.36	117.01	254.26	266.45	84.11				
AA456687_at	AA456687	1197	EST	3.08	0.01189	17.88	37.03	53.32	130.65	118.55	65.44				
rc_AA456845_at	AA456845	1198	KIAA0680 gene product	#N/A	#N/A	23.95	17.11	17.99	67.15	63.46	49.27				
rc_AA458652_at	AA458652	1202	EST	8.26	0.00001	19.3	18.21	17.18	203.23	218.67	53.52				
rc_AA459005_at	AA459005	1210	EST	#N/A	#N/A	-3.57	12.22	40.05	49.76	42.58	28.85				
rc_AA459256_at	AA459256	1212	lectin, mannose-binding, 1	3.01	0.00094	3.83	8.1	8.32	65.91	63.36	39.92				
rc_AA460661_at	AA460661	1229	EST	7.02	0.00053	-1.52	-6.03	15.81	184.62	198.21	108.17				
rc_AA461448_at	AA461448	1240	EST	#N/A	#N/A	1.74	-4.19	22.52	58.65	56.06	32.42				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			normal			normal		
			In metas	p value	c: Median	c: Mean	Median	Dev	c: Std	set 2: Mean	Median	Std Dev	set 2: Median	Std Dev
rc_AA463729_at	AA463729	1250 EST	4.07	0.00676	19.31	19.05	13.37	150.62	116.86	156.67				
rc_AA463876_at	AA463876	1252 EST	3.31	0.00109	9.81	11.89	10.39	73.95	73.76	46.64				
rc_AA464606_at	AA464606	1261 MRS1 protein	#N/A	#N/A	24.35	19.03	39.62	59.55	36.75	57.76				
rc_AA465381_at	AA465381	1272 EST	#N/A	#N/A	88.83	36.24	130.22	102.73	113.07	52.43				
rc_AA465720_at	AA465720	1274 EST	#N/A	#N/A	11.5	21.33	37.22	93.06	108.97	43.26				
solute carrier family 21 (organic anion transporter),														
rc_AA470153_at	AA470153	1275 member 9	13.26	0.00315	47.49	48.57	116.54	726.75	713.23	297.62				
homolog of mouse quaking QKI (KH domain RNA binding protein)														
rc_AA478104_at	AA478104	1296	#N/A	#N/A	-7.07	-11.44	23.2	62.06	47.17	56.07				
rc_AA478441_at	AA478441	1302 cathepsin F	5.07	0.00752	53.85	67.48	43.52	243.44	243.61	69.17				
rc_AA479148_at	AA479148	1311 EST	38.05	0	6.2	1.32	14.38	895.91	847.72	362.53				
rc_AA479266_at	AA479266	1312 EST	#N/A	#N/A	18.04	21.7	25.73	42.53	38.32	18.46				
S-adenosylhomocysteine hydrolase-like 1														
rc_AA479488_at	AA479488	1313	4	0.0269	75.18	60.93	59.8	241.1	222.96	112.87				
rc_AA479961_at	AA479961	1320 EST	#N/A	#N/A	33.49	28.45	10.58	88.13	89.35	36.9				
rc_AA479968_s_at	AA479968	1321 arylsulfatase A	9.01	0.00224	37.97	20.36	45.8	331.32	312.63	97.49				
rc_AA480991_s_at	AA480991	1323 EST	8.59	0.00156	48.08	25.74	51.03	444.29	309.38	367.89				
MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)														
rc_AA480997_l_at	AA480997	1324	#N/A	16	20.58	9.93	68.53	55.62	63.6					
rc_AA481057_f_at	AA481057	1325 EST	#N/A	#N/A	16.3	18.55	8.1	33.83	37.89	23.22				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change		metastat1		metastat1		normal		normal	
			In metas	p value	c: Mean	c: Median	c: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	set 2: Mean	set 2: Median
rc_AA486407_at	AA486407	1347 EST	#N/A	33.22	47.88	28.61	81.72	97.02	55.07	55.07	98.76	95.59
rc_AA486567_at	AA486567	1350 EST	5	0.00002	4.65	2.5	21.62	131.53	98.76	95.59	131.53	98.76
rc_AA486794_at	AA486794	1351 EST	#N/A	#N/A	49.57	52.25	18.73	78.8	72.55	31.84	72.55	78.8
rc_AA487195_at	AA487195	1354 EST	#N/A	#N/A	8.73	7.94	9.21	21.04	14.67	16.52	21.04	14.67
rc_AA487503_at	AA487503	1356 EST	8.85	0.00012	13.8	17.99	8.76	220.45	255.47	119.11	220.45	17.99
rc_AA487576_at	AA487576	1357 EST	#N/A	#N/A	-12.17	-14.87	17.17	26.05	25.27	11.13	26.05	-14.87
rc_AA489009_at	AA489009	1366 EST	#N/A	#N/A	15.19	18.01	8.67	59.19	45.15	41.42	59.19	18.01
rc_AA490882_s_at	AA490882	1381 EST	3.29	0.00319	20.67	13.84	27.06	100.67	98.47	54.46	100.67	13.84
rc_AA490890_at	AA490890	1382 EST	3.02	0.00007	20.26	21.34	9.23	75.61	65.02	33.37	75.61	21.34
rc_AA490947_at	AA490947	1383 EST	#N/A	#N/A	34.15	35	21.49	56.24	38.75	49.85	56.24	35
rc_AA490964_at	AA490964	1384 EST	#N/A	#N/A	20.3	17.53	11.39	47.7	41.84	25.18	47.7	11.39
rc_AA495803_at	AA495803	1392 EST	#N/A	#N/A	95.29	83.46	90.72	94.07	93.85	37.65	93.85	83.46
rc_AA495924_at	AA495924	1395 kinesin family member 3B	#N/A	#N/A	4.16	3.28	2.95	35.69	34.43	19.93	35.69	2.95
rc_AA496053_at	AA496053	1396 EST	3.28	0.00095	5.36	2.22	17.58	81.79	94.01	42.77	81.79	5.36
rc_AA496227_at	AA496227	1402 EST	#N/A	#N/A	24.89	26.85	9.47	58.2	58.42	17.68	58.2	26.85
rc_AA496936_at	AA496936	1403 EST	#N/A	#N/A	17.71	9.86	20.19	30.24	34.4	14.77	30.24	9.86
rc_AA504324_at	AA504324	1412 EST	#N/A	#N/A	45.99	38.81	31.27	74.31	72.05	31.59	74.31	38.81
rc_AA521290_at	AA521290	1421 EST	4.53	0.0148	46.54	22.84	63.63	166.84	174.65	58.28	166.84	22.84
rc_AA598412_at	AA598412	1425 EST	#N/A	#N/A	-2.4	-5.93	29.83	59	52.53	29.41	59	29.83
rc_AA598453_s_at	AA598453	1429 EST	#N/A	#N/A	7.27	7.06	9.67	67.15	54.25	41.65	67.15	7.06
rc_AA598685_at	AA598685	lectin, galactoside-binding,	#N/A	#N/A	16.45	11.35	11.87	55.9	55.08	42.18	55.9	11.87
rc_AA599107_at	AA599107	soluble, 8 (galectin 8)	#N/A	#N/A	53.34	10	88.85	77.28	58.08	40.75	77.28	10
rc_AA599199_at	AA599199	1444 enzyme 1	#N/A	#N/A	187.77	108.97	225.55	695.29	680.26	375.12	695.29	108.97
rc_AA599214_at	AA599214	1446 EST	#N/A	#N/A	10.94	7.36	12.27	34.58	36	14.54	34.58	7.36

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			metastatic			normal		
			In metas	p value	c: Mean	c: Median	c: Std Dev	set 2: Median	set 2: Std Dev	set 2: Mean	set 2: Std Dev	normal	normal	normal
rc_AA599365_at	AA599365	1449 decorin	#N/A	#N/A	36.41	34.43	21.53	83.84	84.81	43.41				
rc_AA600248_at	AA600248	1461 EST	#N/A	#N/A	59.91	32.47	80.55	71.14	61.42					
rc_AA608546_at	AA608546	1463 EST	12.52	0.00003	-19.59	-29.07	29.39	310.07	300.44	189.6				
rc_AA608723_at	AA608723	1467 EST	#N/A	#N/A	17.44	15.29	13.31	66.54	70.38	20.94				
rc_AA609316_at	AA609316	1481 EGF-like-domain, multiple 5	7.97	0.00011	22.6	21.61	25.56	236.54	226.79	65.9				
rc_AA609519_at	AA609519	1482 EST	8.13	0.00009	29.3	22.08	22.59	261.82	243.76	105.33				
rc_AA609715_at	AA609715	1488 EST	#N/A	#N/A	-1.49	-3.92	10.63	29.09	33.14	17.26				
NOT3 (negative regulator of transcription 3, yeast)			#N/A	#N/A	4.34	8.96	16.51	48.05	40.77	32.06				
rc_AA620965_at	AA620965	1511 homolog												
rc_AA621209_at	AA621209	1516 elegans protein C42C1.9	6.34	0.00144	22.77	19.95	46.78	214.61	167.05	138.24				
rc_AA621235_at	AA621235	1517 EST	3.44	0.0021	26.29	24.68	23.17	114.75	113.36	65.35				
rc_AA621315_at	AA621315	1521 like 1	#N/A	#N/A	191.28	141.04	182.69	313.23	281.93	134.57				
rc_AA621796_at	AA621796	1531 kinesin family member 3B	4.44	0.00032	21.81	23.64	8.64	128.01	124.81	70.04				
AB000114_at	AB000114	1532 osteomodulin	#N/A	#N/A	-2.62	-0.81	29.14	31.94	25.4	20.87				
Homogenotate 1,2-dioxygenase (homogenotate 1,2-dioxygenase)														
AF000573_maf_at	AF000573	13.76 0.00002	9.05	13.23	17.33	380.3	348.9	256.4						

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			metastatic			normal		
			In metas	p value	c: Median	c: Mean	c: Std Dev	c: Median	c: Mean	c: Std Dev	c: Median	set 2: Mean	set 2: Median	set 2: Std Dev
solute carrier family 4, sodium bicarbonate cotransporter, member 4														
AF007216_at	AF007216	1550 sodium bicarbonate cotransporter, member 4	5.79	0.00005	14.85	9.84	13.93	157.72	162.44	99.26				
C02532_at	C02532	1563 EST	#N/A	0.12	16.41	16.79	32.27	34.25	11.02					
C15871_at	C15871	1575 EST	3.26	0.00046	13.83	18.19	16.99	79.77	83.41	40.17				
C16420_s_at	C16420	1576 EST	5.95	0.00119	26.92	20.84	24.82	205.53	234.17	120.92				
C18029_at	C18029	1577 tumor susceptibility gene 101	#N/A	0.00001	27.46	26.72	26.09	94.81	95.79	33.89				
rc_C20653_at	C20653	1578 EST	10.59	7.99	2.12	11.85	251.82	299.09	106.09					
aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)														
rc_C20982_at	C20982	1582 EST	#N/A	68.8	85.38	28.73	104.44	88.12	66.28					
rc_C21130_at	C21130	1583 EST	8.79	0.00008	17.56	8.6	19.19	277.18	238.8	188.55				
rc_D11802_at	D11802	1597 angiotensinogen	5.65	0.00009	55.88	52.43	25.14	319.73	291.02	132.07				
low density lipoprotein receptor (familial hypercholesterolemia)														
rc_D11835_at	D11835	1598 hypercholesterolemia	21.76	0.00307	76.38	23.21	131.25	895.7	910.39	322.98				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in metas	p value	metastatic			normal			normal		
					c: Mean	c: Median	c: Std Dev	c: Mean	c: Median	c: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev
phosphodiesterase I/nucleotide													
D12485_at	D12485	1600 (homologous to mouse Ly-41 antigen)	4.57	0.00008	-2.69	-0.53	9.86	101.7	90.07	48.62			
cytochrome P450, subfamily IVF, polypeptide 2, cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase)													
D12620_s_at	D12620	1601	35.09	0.00015	41.08	36.71	10.11	604.7	631.98	249.32			
D13243_s_at	D13243	1602 RBC	20.22	0	-35.85	-34.85	51.7	579.28	445.53	502			
angiotensin receptor 1, angiotensin receptor 1B (HGF activator)													
D13814_s_at	D13814	1611	3.12	0.00101	13.86	10.01	12.82	79.69	75.71	45.03			
D14012_s_at	D14012	1612	12.75	0.0035	160.15	216.05	107.03	1705.96	1963.23	794.42			
D14664_at	D14664	1616 KIAA0022 gene product	8.98	0.00011	14.15	13.51	9.07	233.08	248.97	111.44			
aminomethyltransferase (glycine cleavage system protein T)													
D14686_at	D14686	1617	#N/A	#N/A	76.93	90.12	29.68	171.07	190.08	34.32			
D14695_at	D14695	1618 KIAA0025 gene product; MMS-inducible gene	6.48	0	28.53	28.21	12	196.04	197.12	77.25			

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastat1			metastat1			normal		
			in metas	p value	c: Median	c: Std Dev	c: Std Dev	set 2: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	normal Std Dev	normal Std Dev	normal Std Dev
D16350_at	D16350	SA (rat hypertension-associated) homolog	3.83	0.00117	27.34	29.05	12.27	128.95	133.42	133.42	74.27			
D16626_at	D16626	histidine ammonia-lyase	22.66	0	11.74	8.13	16.04	538.78	535.2	535.2	166.14			
D16626_at	D16626	histidine ammonia-lyase	22.66	0	12.06	22.91	55.95	289.6	256.22	256.22	113.59			
D31716_at	D31716	basic transcription element binding protein 1	5.35	0.00086	16.08	23.65	17.64	166.06	203.79	203.79	87.22			
D31815_at	D31815	regucalcin (senescence marker protein-30)	10.55	0.00037	11.48	10.25	7	298.48	281.03	281.03	183.56			
D45288_at	D45288	EST	#N/A	#N/A	-19.35	-33.07	27.77	31.63	32.56	32.56	42.02			
rc_D45529_at	D45529	EST	3.82	0.00193	12.24	-3.36	29.18	126.63	109.06	109.06	70.64			
rc_D45714_at	D45714	EST	5.64	0.00384	34.3	29.86	13.09	301.07	218.14	218.14	282.7			
D49742_at	D49742	hyaluronan-binding protein 2	18.13	0.00012	11.38	-0.72	41.45	509.66	531.78	531.78	127.5			
D50312_at	D50312	potassium inwardly-rectifying channel, subfamily J, member 8	#N/A	#N/A	-2.39	3.94	24.71	76.55	72.56	72.56	48.96			
D50582_at	D50582	potassium inwardly-rectifying channel, subfamily J, member 11	#N/A	#N/A	61.44	65.47	28.34	70.38	76.35	76.35	25.4			
rc_D56989_f_at	D56989	EST	#N/A	#N/A	8.83	6.61	9.79	77.62	55.56	55.56	72.14			

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change			metastati			normal		
				In metas	p value	c: Median	c: Mean	c: Std Dev	c: Median	c: Std Dev	set 2: Median	set 2: Std Dev
D57823_at	D57823	1690	Sec23 (S. cerevisiae)	4.43	0	13.37	13.08	8.38	94.25	87.66	30.56	
D57916_s_at	D57916	1691	EST	#N/A	#N/A	67.05	42.08	79.49	126.25	103.85	69.38	
rc_D59294_at	D59294	1693	EST	#N/A	#N/A	1.31	0.89	6.58	22.83	20.84	14.1	
rc_D59554_f_at	D59554	1698	EST	6.7	0	6.09	9.79	34.83	184.48	158.33	79.55	
rc_D60769_s_at	D60769	1703	KIAA0096 protein	4.31	0.00142	13.44	13.91	10.95	119.96	107.2	86.36	
D61991_at	D61991	1706	EST	4.84	0.00005	22.03	21.01	10.8	131.66	150.48	60.06	
D62103_s_at	D62103	1707	EST	4.11	0.0263	96.52	111.02	79.07	349.4	258.95	229.11	
			ficolin (collagen/fibrinogen domain-containing lectin) 2									
D63160_at	D63160	1709	(fucolin)	4.01	0.00391	51.13	46.11	30.07	219.26	228.53	125.06	
D76435_at	D76435	1716	Zic family member 1 (odd-paired Drosophila homolog)	#N/A	#N/A	7.52	9.44	7.51	28.48	22.05	16.54	
D78011_at	D78011	1717	dihydropyrimidinase	21.37	0.00003	22.34	11.34	31.83	640.3	680.03	206.48	
			sterol-C5-desaturase (fungal ERG3, delta-5-desaturase)-like									
D85181_at	D85181	1750		9.56	0.00005	31.54	25.11	23.09	350.04	388.34	151.37	
D85433_at	D85433	1751	EST	#N/A	#N/A	45.14	48.1	33.75	45.46	44.56	22.01	
D86983_at	D86983	1758	p53-responsive gene 2	#N/A	#N/A	44.18	43.24	14.93	56.19	53	16.12	
			solute carrier family 23 (nucleobase transporters), member 1									
D87075_at	D87075	1760	member 1	4.15	0.00067	5.77	-0.83	26.24	119.77	104.75	72.62	

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastat! c: Std Dev			normal set 2: Median			normal set 2: Std Dev		
			In metas	p value	c: Mean	metastat!	c: Std	metastat!	c: Std	normal	Median	normal	Median	normal
D90042_at	D90042	N-acetyltransferase 2 (arylamine N- acetyltransferase)	7.06	0	5.13	18.92	32.5	167.38	176.16	66.7				
D90282_at	D90282	carbamoyl-phosphate synthetase 1, mitochondrial	27.29	0.00002	8.24	12.24	8.02	712.98	819.32	415.69				
rc_F04611_at	F04611	EST	23.96	0.00018	42.65	18.88	62.74	1011.12	1040.46	589.37				
rc_F04677_at	F04677	EST	#N/A	#N/A	138.06	123.28	34.39	355.75	310.97	168.21				
rc_F04944_s_at	F04944	acyl-Coenzyme A oxidase	4.01	0.00242	40.92	33.99	28.07	191.04	192.25	99.98				
rc_F09350_at	F09350	EST	4.79	0.00088	13.91	-6.46	33.97	147.64	130.28	79.24				
rc_f09687_s_at	F09687	EST	#N/A	#N/A	12.72	8.26	28.12	58.85	57.03	31.82				
rc_F09729_at	F09729	EST	#N/A	#N/A	9.35	20.58	23.17	55.49	55.78	27.37				
rc_F09979_at	F09979	EST	4.36	0.02555	6.98	6.51	20.72	226.47	116.41	288.21				
rc_F10149_at	F10149	EST	#N/A	#N/A	11.86	108.46	60.06	257.05	276.87	165.09				
rc_F10276_s_at	F10276	dual specificity phosphatase 6	8.13	0.0001	19.64	13.06	12.33	240.65	275.65	138.17				
butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase)														
rc_F10380_at	F10380	hydroxylase	#N/A	#N/A	36.92	34.01	13.56	106.49	93.71	83.35				
rc_F10381_s_at	F10381	KIAA0541 protein	#N/A	#N/A	22.16	25.03	8.75	64.94	71.82	26.24				
rc_F10418_at	F10418	EST	#N/A	#N/A	44.91	44.45	22.72	64.3	52.54	31.96				
rc_F10874_f_at	F10874	EST	4.19	0.00025	233.85	209.96	107.99	1016.95	990.04	477.31				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in metas		p value	c: Mean	Median	c: Std Dev	metastati	c:	Median	normal	set 2: Median	normal	set 2: Median	normal	set 2: Median		
			#N/A	#N/A															
rc_F13624_at	F13624	breast cancer anti-estrogen resistance 3	#N/A	#N/A	27.76	19.2	32.49	90.8	73.79	90.8	73.79	59.27							
rc_F13782_s_at	F13782	LIM binding domain 2	4.17	0.00109	-0.64	5.61	22.4	100.8	119.01	100.8	119.01	55.07							
		solute carrier family 16 (monocarboxylic acid transporters), member 4	#N/A	#N/A	9.13	9.22	13.53	32.73	34.27	32.73	34.27	21.05							
rc_H01059_l_at	H01059	1830	5.96	0.00458	5.06	1.15	14.13	261.57	93.25	261.57	93.25	407.93							
rc_H02855_at	H02855	EST	5.77	0.0001	1.48	7.75	17.79	135.1	134.05	135.1	134.05	75.43							
rc_H03348_at	H03348	claudin 1	#N/A	#N/A	9.16	12.81	14.19	68.16	65.08	68.16	65.08	40.19							
rc_H05970_at	H05970	EST	#N/A	#N/A	313.2	309.79	122.67	512.04	486.42	309.79	122.67	486.42	149.27						
rc_H09331_f_at	H09331	EST	23.06	0.00094	45.11	18.95	65.29	782.6	824.74	45.11	65.29	824.74	226.28						
rc_H09353_at	H09353	EST	4.54	0.00276	31.29	18.75	28.5	132.09	124.86	31.29	18.75	132.09	64.37						
		glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P)	10.33	0.00023	-21.2	-37.69	28.32	290.05	210.37	-21.2	-37.69	28.32	290.05	210.37	244.67				
rc_H11739_s_at	H11739	1876	10.72	0.0056	39.96	-9.15	111.74	515.58	506.07	39.96	-9.15	111.74	515.58	506.07	224.5				
		zinc-finger protein 265	#N/A	#N/A	45.29	37.73	26.92	87.28	94.49	#N/A	37.73	26.92	87.28	94.49	38.15				
rc_H12593_at	H12593	EST	#N/A	#N/A	12.2	9.54	8.57	31.08	31.66	#N/A	9.54	8.57	31.08	31.66	13.28				
rc_H16098_at	H16098	EST	#N/A	#N/A	76.83	44.82	89.14	76.54	74.4	#N/A	76.83	44.82	89.14	76.54	74.4	40.21			
rc_H17472_s_at	H17472	EST	#N/A	#N/A	7.63	4.09	6.45	227.6	225.23	#N/A	7.63	4.09	227.6	225.23	227.6				
rc_H19089_at	H19089	EST	3.13	0.04948	77.07	49.48	64.05	227.6	225.23	77.07	49.48	64.05	227.6	225.23					

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastat1 c: Std			normal set 2: Median			normal set 2: Std Dev				
			In metas	p value	c: Mean	metastat1 Median	c: Std Dev	normal Mean	normal Std Dev	normal Median	normal Std Dev	normal Mean	normal Std Dev	normal Median	normal Std Dev	
protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform																
rc_H57850_at	H57850	1958	3.02	0.00123	41.36	36.05	15.14	131.12	130.36	53.67						
rc_h58692_s_at	H58692	1960	81.41	0	-2.66	5.46	16.1	1886.69	1520.43	1129.35						
rc_H60317_at	H60317	1965	#N/A	#N/A	18.86	22.34	11.81	38.92	39.1	18.67						
H61002_at	H61002	1967	#N/A	#N/A	68.96	23.38	102.25	88.87	93.79	36.34						
H66367_at	H66367	1977	6.68	0.0001	-5.44	-2.13	18.66	155.38	149.31	70.77						
rc_H68239_f_at	H68239	1983	#N/A	#N/A	26.96	17.94	15.81	66.76	66.18	51.67						
v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog																
rc_H69138_at	H69138	1986	6.76	0.00142	42.88	30.87	38.35	328.51	313.13	218.8						
rc_H69565_at	H69565	1987	4.11	0.00002	15.45	16.92	9.4	95.6	94.91	42.92						
rc_H70485_at	H70485	1988	#N/A	#N/A	113.44	81.62	63.73	232.9	256.86	107.1						
rc_H70554_at	H70554	1989	10.99	0	-11.73	-19.98	33.09	292.66	288.78	153.17						
rc_H70627_s_at	H70627	1990	#N/A	#N/A	17.89	17.62	8.85	42.72	41.34	11.7						
H72650_at	H72650	1994	EST	#N/A	81.21	98.79	41.38	122	125	42.24						
rc_H73535_s_at	H73535	1996	EST	6.89	0.00202	154.24	97.36	149.45	912.39	956.58	383.35					
rc_H77494_at	H77494	1999	EST	#N/A	9.65	6.64	15.53	42.67	47.73	27.54						
rc_H79820_at	H79820	2004	EST	3.25	0.01466	10.64	2	22.28	113.3	113.19	95.96					
rc_H81070_f_at	H81070	2006	RNA helicase-related protein	25.74	0.00126	93.43	62.01	121.29	2044.42	2051.11	615.84					
rc_H81964_s_at	H81964	2008	SEC14 (S. cerevisiae)-like 1	#N/A	#N/A	9.95	15.7	12.54	29.9	21.14	20.56					
rc_H82424_at	H82424	2009	EST	#N/A	#N/A	41.99	48.17	21.1	65.11	69.41	36.73					

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change			metastatic			normal			normal	
				In metas	p value	c: Std Dev	c: Mean	c: Median	c: Std Dev	set 2: Median	set 2: Std Dev	set 2: Median	set 2: Std Dev	
NOT3 (negative regulator of transcription 3, yeast)														
rc_H82735_s_at	H82735	2010	homolog	#N/A	#N/A	-1.13	6.14	29.78	58.77	54.86	35.76			
rc_H82966_s_at	H82966	2011	apolipoprotein B (including Ag(x) antigen)	3.42	0.00769	0.2	1	15.26	100.93	77.36	96.78			
rc_H83109_f_at	H83109	2012	EST	16.55	0.00001	2.74	4.43	21.21	417.46	421.97	224.35			
rc_H87765_at	H87765	2017	KIAA0626 gene product, protein phosphatase 1, regulatory (inhibitor) subunit	3.86	0.00131	5.2	7.91	19.6	94.26	93.78	60.64			
rc_H89980_at	H89980	2026	5	31.13	0.00006	12.16	13.82	12.3	990.48	1005.21	755.6			
rc_H90417_s_at	H90417	2028	EST	4.17	0.015	14.23	-10.79	70.02	191.04	154.37	125.5			
rc_H93381_at	H93381	2036	EST	24.23	0	6.08	-0.69	28.81	621.48	640.77	214.25			
rc_H93562_at	H93562	2038	homolog	3.17	0.00113	20.83	14.13	20.46	89.3	84.36	37.72			
rc_H93745_s_at	H93745	2040	GS2 gene	#N/A	#N/A	4.52	8.01	8.31	47.92	46.53	28.87			
rc_H95079_at	H95079	2046	EST	#N/A	#N/A	7.05	11.03	7.33	39.79	33.3	29.08			
rc_H95089_at	H95089	2047	EST	#N/A	#N/A	13.05	13.54	4.03	31.99	31.89	13.19			
rc_H95358_at	H95358	2049	EST	3.17	0.00182	-5.85	-5.95	11.57	74.74	72.66	42.36			
rc_H95978_at	H95978	2052	EST	8.55	0.00046	12.28	14.38	10.71	240.91	246.43	147.67			
rc_H96392_at	H96392	2053	EST	#N/A	#N/A	12.6	9.93	33.15	35.98	53.46	42.74			
rc_H96897_at	H96897	2056	KIAA0336 gene product	#N/A	#N/A	35.22	19.98	42.05	48.46	50.39	33.36			
rc_H97587_s_at	H97587	2060	endothelin receptor type B	#N/A	#N/A	-5.07	-3.35	14.02	39.65	36.54	21.7			
rc_H97670_at	H97670	2061	EST	#N/A	#N/A	23.31	29.71	31.35	101.35	128.08	56.78			

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			metastatic			normal				
			In metas	p value	: Mean	: Median	: Std Dev	Mean	: Median	: Std Dev	Mean	: Median	: Std Dev	Mean	: Median	: Std Dev
rc_H98083_at	H98083	2067 EST	5.09	0.000025	11.73	11.11	3.97	121.51	104.88	70.52						
rc_H99393_s_at	H99393	2076 endothelin receptor type 3.43	0.000093	4.63	9.33	11.96	79.18	70.67	42.71							

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

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Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			metastatic			normal			normal		
			In metas	p value	c: Mean	c: Median	c: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	
L00389_f_at	L00389	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2	#N/A	#N/A	69.38	86.39	64.81	222.59	184.81	121.16							
L00972_at	L00972	cystathione-beta-synthase	7.19	0.00008	30.44	29.08	21.44	268.9	253.33	153.24							
L04751_at	L04751	cytochrome P450, subfamily IV, polypeptide 11	36.79	0.00004	32.39	23.29	32.64	1164.28	1183.4	334.08							
L07956_at	L07956	glucan (1,4-alpha)-, branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	5.6	0.00029	19.13	18.57	16.75	166.17	184.57	75.67							
L09717_at	L09717	lysosomal-associated membrane protein 2	4.06	0.00034	16.78	9.78	21.83	115.12	111.26	57.66							
L11244_s_at	L11244	complement component 4-binding protein, beta	43.33	0	0.49	-8.84	36.95	1147.16	1114.71	441.14							
L11244_s_at	L11244	complement component 4-binding protein, beta	43.33	0	-13.27	-16.78	12.92	292.9	341.12	114.93							
L11931_at	L11931	hydroxymethyltransferase 1 (soluble)	7.27	0.00041	-18.81	-31.65	26.43	188.25	181.11	114.89							

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			metastatic			normal		
			In metas	p value	c: Mean	c: Median	c: Std Dev	c: Mean	c: Std Dev	c: Mean	c: Std Dev	set 2: Median	set 2: Std Dev	
L13689_at	L13689	murine leukemia viral (bmi-1) oncogene homolog activating transcription factor	#N/A	#N/A	32.33	34.76	18.57	63.42	77.84	36.39				
L19871_at	L19871	2164 3	#N/A	#N/A	72.2	31	78.72	98.22	85.66	61.41				
L26336_at	L26336	2185 heat shock 70kD protein 2	#N/A	#N/A	15.67	14.08	10.72	31.12	33.86	10.1				
L27050_at	L27050	2186 apolipoprotein F	10.26	0.00026	-23.8	-20.7	14.43	258.1	252.65	124.08				
L27841_at	L27841	2187 pericentriolar material 1	#N/A	#N/A	58.75	58.95	40.61	90.06	82.71	28.43				
L32140_at	L32140	2192 afamin	17.31	0.00003	9.44	16	10.75	426.89	464.97	221.11				
L32179_at	L32179	arylacetamide deacetylase (esterase)	23.83	0	22.94	24.96	16.06	688.97	675.71	305.75				
L32961_at	L32961	4-aminobutyrate aminotransferase	#N/A	#N/A	15.64	7.44	15.63	76.44	79.62	26.55				
L33799_at	L33799	2196 endopeptidase enhancer	#N/A	#N/A	87.45	73.5	89.14	230.54	248.1	130.08				
		bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choleoyltransferase)												
L34081_at	L34081	2199	11.96	0.00008	6.09	4.41	14.12	314.27	330.42	174.43				
L41067_at	L41067	2213 cells, cytoplasmic 3	4.96	0.00473	57.54	60.41	36.65	261.77	228.95	110.65				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic metastatic			normal			normal			
			In metas	p value	c: Mean	c: Median	c: Std Dev	c: Mean	c: Std Dev	set 2: Median	set 2: Mean	set 2: Std Dev	set 2: Median	set 2: Mean	set 2: Std Dev
L41067_at	L41067	nuclear factor of activated T- cells, cytoplasmic 3	4.96	0.00473	30.25	13.66	32.44	73.87	77.38	52.02					
L44424_at	L44424	#N/A	2213	UIMP-CMP kinase	23.79	18.2	26.85	57.57	43.3	36.92					
L48516_at	L48516	paraoxonase 3	22.21	0.00004	36.05	28.85	37.25	896.92	896.69	337.05					
M10058_at	M10058	astagal glycoprotein receptor 1	23.96	0	-47.64	-42.75	75.52	591.6	603.68	188.25					
M10943_at	M10943	metallothionein 1F (functional)	3.88	0	53.15	52.73	8.81	217.65	186.71	86.73					
M11437_cds1_at	M11437	kininogen	18.38	0.00006	20.84	10.7	36.84	535.53	539.53	186.97					
M11567_mra1_at	M11567	anglogenin, ribonuclease, RNase A family, 5	32.25	0.0001	2.5	-18.19	58.03	1019.17	968.25	273.9					
M12625_at	M12625	lecithin-cholesterol acyltransferase	4.55	0.01584	110.15	128.06	73.94	447.22	425.61	138.52					
M12712_s_at	M12712	protein C (inactivator of coagulation factors Va and VIIIa)	7.37	0.01866	107.12	177.74	113.63	646.94	628.19	326.15					
M12759_at	M12759	EST	#N/A	#N/A	27.23	21.91	28.99	97.65	103.06	53.91					
M13143_at	M13143	kallikrein B plasma, Fletcher factor 1	10.39	0.00019	38.55	37.19	32.81	402.05	441.15	122.27					
M13232_s_at	M13232	coagulation factor VII (serum prothrombin conversion accelerator)	5.9	0.00014	43.46	42.59	18.46	248.65	275.82	70.94					
M13699_at	M13699	ceruloplasmin (ferroxidase)	15.85	0.00012	36.21	37.43	44.51	688.89	638.74	329.28					

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			metastatic			normal		
			In metas	p value	c: Mean	c: Median	c: Std Dev	c: Mean	c: Median	c: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	
M22324_at	M22324	aminopeptidase N, aminopeptidase M, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	#N/A	#N/A	224.68	25.21	471.53	365.81	363.02	134.32				
M23234_s_at	M23234	ATP-binding cassette, sub-family B (MDR/TAP), member 4	10.05	0	-4.37	-11.49	29.05	255.03	242.93	112.08				
M24283_at	M24283	Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor acyl-Coenzyme A dehydrogenase, C-2 to C-3	3.19	0.04985	77.88	34.05	69.45	207.07	183.74	121.4				
M26393_s_at M29194_at	M26393 M29194	short chain lipase, hepatic	16.27	0.00007	16.81	12.39	48.16	677.3	775.54	358.47				
M30185_at	M30185	12.18 cholesteryl ester transfer protein, plasma	3.83	0.0013	-37.15	-29.18	28.09	93.07	86.04	61.35				
M30257_s_at M30269_at	M30257 M30269	vascular cell adhesion molecule 1 nitrogen (enactin)	3.11	0.00064	17.33	13.46	10.06	78.1	82.04	35.74				
			3.4	0.00026	19.81	26.36	14.57	96.8	94.16	42.52				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			normal		
			In metas	P value	c: Mean	c: Median	c: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	
M33317_f_at	M33317	cytochrome P450, subfamily II A (phenobarbital-inducible), polypeptide 7	32.63	0	44.53	35.06	29.77	1613.89	1437.34	1086.43	
M61853_at	M61853	cytochrome P450, subfamily II C (mephenytoin 4-hydroxylase), polypeptide 18	7.82	0.00024	12.17	12.44	4.36	191.94	204.27	91.68	
M61854_s_at	M61854	cytochrome P450, subfamily II C (mephenytoin 4-hydroxylase)	3.3	0.04185	52.7	55.56	44.01	321.6	166.36	430.71	
M63967_at	M63967	aldehyde dehydrogenase 5	4.04	0.00058	34.59	36.64	5.46	164.38	178.74	87.39	
M64174_at	M64174	Janus kinase 1 (a protein tyrosine kinase)	#N/A	#N/A	10.42	10.81	15.82	59.51	59.38	27.77	
M64554_maf1_at	M64554	coagulation factor XIII, B	5.87	0.00011	-4.73	-4.91	7.92	137.26	136.8	72.05	
M64590_at	M64590	glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P)	6.41	0.00002	14.28	17.87	8.65	152.26	127.72	82.96	

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastat1 c: Median			metastat1 c: Std Dev			normal set 2: Mean			normal set 2: Std Dev		
			In metas	p value	c: Mean	metastat1 c: Median	metastat1 c: Std Dev	metastat1 c: Std	metastat1 c: Mean	metastat1 c: Std Dev	metastat1 c: Std	normal set 2: Mean	normal set 2: Std Dev	normal set 2: Mean	normal set 2: Std Dev		
Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform																	
M64929_at	M64929	2383 complement component 5 protein C inhibitor (plasminogen activator inhibitor III)	#N/A	#N/A	64.63	38.82	95.31	106.38	88.13	67.95	67.95						
M65134_s_at	M65134	2385 complement component 5 protein C inhibitor (plasminogen activator inhibitor III)	12.01	0.00012	2.31	3.66	7.43	303.27	337.95	151.33	151.33						
M68516_ma1_at	M68516	2387 monoamine oxidase A	20.54	0	-1.34	-11.78	20.54	466.81	481.06	119.75	119.75						
M68840_at	M68840	2388 monoamine oxidase B	3.96	0.01396	42.09	28.9	45.52	182	201.64	94.09	94.09						
M69177_at	M69177	2392 transcription factor 4 carboxypeptidase B2	11.64	0.00001	21.97	20.41	20.83	322.15	340.27	94	94						
M74719_at	M74719	2396 plasma	#N/A	#N/A	8.97	15.15	10.62	46.89	44.78	12.66	12.66						
M75106_at	M75106	2397 (plasma)	40.63	0	19.77	30.19	22.24	1170.81	1124.59	329.77	329.77						
Hydroxysteroid (11-beta) dehydrogenase 1																	
M76665_at	M76665	2398 caldesmon 1	19.22	0.00004	33.41	17.51	23.86	628.97	670.88	196.22	196.22						
M83216_s_at	M83216	2407 flavin containing monooxygenase 3	4.27	0.00037	7.89	2.98	12.17	105.21	109.38	55.62	55.62						
M83772_at	M83772	2409 plasminogen,plasminogen-like	19.54	0	6.88	-0.95	15.39	504.14	595.51	245.03	245.03						
M86873_s_at	M86873	2414 like	17.54	0	-3.92	-8.08	6.71	410.11	403.69	218.51	218.51						

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastati c:			normal set 2: Mean			normal set 2: Median			normal set 2: Std Dev		
			In metas	P value	c: Mean	c: Std	Median	Dev	Mean	Median	Dev	Mean	Median	Dev	Mean	Median	Dev
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1																	
M88163_at	M88163	2416 regulator of chromatin, subfamily a, member 1	3.37	0.00098	17.39	17.52	7.25	84.41	91.86	91.86	41.42						
M88338_at	M88338	2417 serum constituent protein mevalonate kinase	#N/A	#N/A	134.22	128.76	53.79	155.51	140.27	140.27	70.28						
M88468_at	M88468	2418 (mevalonic aciduria) methylmalonate-semialdehyde dehydrogenase	#N/A	#N/A	89.85	108.13	54.23	214.81	260.33	260.33	86.76						
M93405_at	M93405	2424 dehydrogenase dihydroorotate	23.06	0	16.51	27.77	20.66	679.66	734.58	734.58	307.25						
M94065_at	M94065	2425 dehydrogenase	6.47	0.00013	30.26	20.14	17.64	202.13	183.44	183.44	86.43						
M95767_at	M95767	2432 chitobiase, di-N-acetyl-	4.94	0.00004	26.01	37.13	21.53	173.07	153.03	153.03	95						
CD36 antigen (collagen type I receptor, thrombospondin receptor)																	
M98399_s_at	M98399	2437 receptor	#N/A	#N/A	4.71	4.58	5.51	47.65	38.28	38.28	35.2						
rc_N21626_at	N21626	2445 EST	#N/A	#N/A	29.77	24.63	25.09	59.18	46.15	46.15	33.56						
rc_N22404_at	N22404	2450 EST	3.99	0.01152	30.59	23.97	55.32	193.63	130.09	130.09	162.83						
rc_N22434_at	N22434	2451 EST	4.37	0.01725	100.96	66.55	110.62	334.51	328.98	328.98	150.7						
rc_N22938_s_at	N22938	2453 serum amyloid A4,	35.39	0.00128	163.4	145.31	160.24	4244.44	3330.35	3330.35	2358.25						
rc_N24879_at	N24879	2460 EST	9.44	0.00008	6.2	5.49	23.52	280.93	337.77	337.77	165.77						

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change in metas		metastati p value		c: Mean		metastati c: Median		normal set 2: Median		normal set 2: Std Dev			
				#N/A	#N/A	#N/A	#N/A	c: Std Dev	c: Std Dev	Mean	Median	Mean	Median	Std Dev	Std Dev		
rc_N24973_at	N24973	2462	EST	3.13	0.00216	14.18	22.08	20.51	87.67	98.26	98.26	98.26	42.62	42.62	22.87	22.87	
rc_N25262_at	N25262	2465	EST							64.13	64.13	64.97	64.97	18.29	18.29		
rc_N27524_at	N27524	2472	EST							28.04	28.04	28.04	28.04	28.04	28.04		
N27670_at	N27670	2474	progesterone membrane binding protein	6.15	0.00321	38.66	15.48	47.19	252.94	292.34	292.34	292.34	292.34	292.34	133.48	133.48	
rc_N29353_at	N29353	2477	(kynurenone 3-hydroxylase)	4.78	0.00019	-4.7	-5.88	13.94	109.79	101.27	101.27	53.38	53.38				
rc_N29543_at	N29543	2479	EST	#N/A	#N/A	11.66	9.07	5.04	59.21	51.22	51.22	30.43	30.43				
rc_N29740_at	N29740	2480	EST	#N/A	#N/A	48.71	27.45	46.9	80.01	77.9	77.9	37.18	37.18				
rc_N31952_at	N31952	2490	EST	3.13	0.01481	36.21	27.5	25.04	133.49	147.66	147.66	83.03	83.03				
rc_N32071_at	N32071	2491	EST	8.75	0.00006	40.89	43.12	15.37	421.21	488.49	488.49	238.4	238.4				
rc_N34804_at	N34804	2497	DKFZP434J214 protein	8.08	0.00028	6.99	5.94	33.73	344.08	176.4	176.4	532.11	532.11				
rc_N34919_at	N34919	2499	EST	#N/A	#N/A	7.39	8	6.82	52.96	44.23	44.23	24.23	24.23				
rc_N35247_at	N35247	2500	EST	#N/A	#N/A	39.9	33.56	15.03	117.08	116.14	116.14	57.05	57.05				
rc_N36085_at	N36085	2505	EST	#N/A	#N/A	20.98	19.21	13.89	58.28	58	58	22.95	22.95				
rc_N40320_at	N40320	2514	EST	7.56	0.01584	99.72	83.43	128.45	558.37	595.16	595.16	250.67	250.67				
rc_N45320_at	N45320	2519	EST	#N/A	#N/A	11.39	11.26	7.06	50.75	36	36	39.19	39.19				
rc_N45998_at	N45998	2520	EST	3.14	0.00337	28.42	22.62	13.52	99.42	110.53	110.53	49.55	49.55				
rc_N47469_at	N47469	2522	EST	3.34	0.00329	20.35	13.91	20.65	104.74	99.87	99.87	61.84	61.84				
rc_N48155_at	N48155	2525	EST	#N/A	#N/A	17.08	16.77	14.66	97.37	54.69	54.69	99.7	99.7				
adaptor-related protein complex 2, mu 1 subunit																	
rc_N48315_at	N48315	2527	complex 2, mu 1 subunit	5.3	0.0149	62.03	30.66	52.29	368.37	331.28	331.28	94.61	94.61				
rc_N48674_at	N48674	2530	EST	4.06	0.00028	2.7	4.57	10.52	72.82	54.62	54.62						
rc_N50038_at	N50038	2541	EST	#N/A	#N/A	0.25	5.19	45.95	47.04	41.45	41.45						

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change			metastat1			metastat1			normal		
				In metas	p value	c: Mean	c: Std Dev	c: Mean	c: Std Dev	set 2: Median	set 2: Std Dev	set 2: Median	set 2: Std Dev	set 2: Median	set 2: Std Dev
rc_N51117_at	N51117	2544	EST	9.68	0.00081	8.23	4.5	11.88	327.53	296.4	266.42	266.42	266.42	266.42	
rc_N52845_at	N52845	2554	EST	5.53	0.00088	28.56	30.14	14.95	219.38	230.31	149.67	149.67	149.67	149.67	
rc_N53757_at	N53757	2560	EST	3.97	0.00255	99.49	80.7	56.09	365.45	324.21	118.42	118.42	118.42	118.42	
rc_N54053_at	N54053	2561	secreted phosphoprotein 2, 24kD	60.39	0.00087	44.3	-18.16	166.47	2749.73	2790.77	1230.33	1230.33	1230.33	1230.33	
rc_N54311_at	N54311	2564	EST	4.82	0.00183	9.77	9.36	25.17	160.29	130.17	124.7	124.7	124.7	124.7	
rc_N54604_at	N54604	2570	EST	3.72	0.00741	2.36	2.08	35.23	133.06	119.1	109.95	109.95	109.95	109.95	
cytidine monophosphate-N-acetylneuraminate hydroxylase (CMP-N-acetylneuraminate hydroxylase)															
rc_N54792_at	N54792	2571	#N/A	3.23	0.00099	28.36	27.42	6.39	110.19	77.69	87.32	87.32	87.32	87.32	
rc_N55272_at	N55272	2574	EST	#N/A	#N/A	22.71	13.6	24.4	45.08	47.45	14.77	14.77	14.77	14.77	
N57464_at	N57464	2576	CCAAT/enhancer binding protein (CEBP), delta	14.69	0.00018	22.28	11.43	38.78	429.29	442.58	169.83	169.83	169.83	169.83	
rc_N57934_s_at	N57934	2577	formiminotransferase cyclodeaminase	13.81	0.00171	806.55	477.9	939.39	9051.2	6373.16	8542.52	8542.52	8542.52	8542.52	
rc_N59089_at	N59089	2581	EST	4.74	0.00055	38.4	36.58	24.6	215.54	167.6	133.64	133.64	133.64	133.64	
rc_N59532_s_at	N59532	2585	aminomethyltransferase (glycine cleavage system protein T)	6.73	0.00005	12.43	2.55	17.66	196.37	155.84	122.13	122.13	122.13	122.13	
rc_N59543_at	N59543	2587	PDZ domain containing 1	9.96	0.00052	1.2	-2.89	17.29	303.49	259.23	225.96	225.96	225.96	225.96	
rc_N59550_at	N59550	2588	EST	25.56	0.00024	19.9	2.53	65.91	855.88	774.72	358.3	358.3	358.3	358.3	

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change			metastatic			metastatic			normal		
				In metas	p value	c: Mean	c: Median	c: Std Dev	c: Mean	c: Std Dev	set 2: Median	set 2: Std Dev	set 2: Median	set 2: Std Dev	
rc_N62523_at	N62523	2592	hepatic leukemia factor	5.02	0.00087	9.04	6.67	16.46	144.8	148.62	85.03	8.24	18.83	8.24	
rc_N62922_at	N62922	2596	EST	#N/A	#N/A	14.92	14.15	2.75	54.94	52.4	124.39	102.9	121.4	121.4	
rc_N63047_at	N63047	2597	EST	#N/A	#N/A	4.13	0.93	9.72	14.78	15.63	8.24	8.24	8.24	8.24	
rc_N63172_at	N63172	2599	cell division cycle 42 (GTP-binding protein, 25kD)	#N/A	#N/A	26.88	33.1	24.75	60.99	57.64	40.01	40.01	40.01	40.01	
rc_N63698_at	N63698	2604	EST	7.92	0.00001	19.14	18.14	12.14	221.25	212.4	122.32	122.32	122.32	122.32	
rc_N64017_at	N64017	2606	EST	5.27	0.00022	5.45	8.71	8.71	122.34	135.27	55.58	55.58	55.58	55.58	
rc_N64436_at	N64436	2609	EST	3.51	0.00441	24.46	20.38	21.08	119.24	133.44	70.66	70.66	70.66	70.66	
rc_N65959_at	N65959	2612	EST	5.43	0.00044	3.51	3.25	22.24	142.87	149.26	79.26	79.26	79.26	79.26	
rc_N66130_at	N66130	2614	progesterone membrane binding protein	3.98	0.0106	29.02	21.05	33.88	172.14	181.78	114.84	114.84	114.84	114.84	
rc_N66613_at	N66613	2617	EST	#N/A	#N/A	25.61	22.34	26.39	62.58	50.13	51.99	51.99	51.99	51.99	
prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler- Scheinker syndrome, fatal familial insomnia)															
rc_N67009_s_at	N67009	2622		3.55	0.00956	25.95	11.35	38.17	122.85	124.39	65.69	65.69	65.69	65.69	
rc_N67105_at	N67105	2624	EST	5.01	0.00176	-0.75	0.21	16.38	143.36	102.9	121.4	121.4	121.4	121.4	
rc_N67876_s_at	N67876	2628	insulin-like growth factor 1 (somatomedin C)	8.89	0.00042	11.81	15.88	8.82	267.41	145.79	238.35	238.35	238.35	238.35	

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastati c:			metastati metastati			normal set 2: set 2:			
			In metas	p value	c: Mean	Median	Dev	#N/A	#N/A	#N/A	15.97	82.1	74.13	59.47	37.21
activating transcription factor 4 (tax-responsive enhancer)															
rc_N67974_at	N67974	2630	4 (tax-responsive element B67)		0.99	0	-6.75	-13.81	19.15	1061.81	1013.27	574.42			
rc_N68133_at	N68133	2633	EST		#N/A	#N/A	4.3	4.02	8.66	34.08	36.71	14.33			
rc_N68596_s_at	N68596	2636	betaine-homocysteine methyltransferase		4.41	0.00078	-13.99	-13.48	10.76	105.8	97.72	72.15			
rc_N68871_at	N68871	2638	EST		#N/A	#N/A									
rc_N70305_at	N70305	2655	EST												
rc_N70358_s_at	N70358	2657	growth hormone receptor kidney- and liver-specific gene		34.35	0	20.93	29.26	36.06	1449.57	1157.97	1115.22			
rc_N71542_at	N71542	2665			21.05	0	-14.76	-18.28	14.3	471.65	486.43	226.63			
rc_n71935_s_at	N71935	2667	multiple PDZ domain protein		16.28	0	12.84	19.17	14.1	410.92	422.1	218.42			
rc_N72200_at	N72200	2669	EST		#N/A	#N/A	12.93	14.15	14.26	57.8	56.14	30.12			
rc_N73561_at	N73561	2676	EST		12.96	0.00011	17.04	4.48	25.06	516.79	458.57	393.69			
rc_N73883_at	N73883	2682	EST		9.35	0	18.47	23.48	17.67	256.78	276.41	95.34			
rc_N74025_at	N74025	2685	deiodinase, iodothyronine, type I		22.79	0	-7.64	2.14	15.95	527.67	515.68	256.99			
rc_N74422_at	N74422	2686	EST		30.32	0	23.57	28.41	36.93	1063.07	1094.48	371.26			
collectin sub-family member															
rc_N74624_at	N74624	2688	10 (C-type lectin)		#N/A	#N/A	33.8	34.24	5.13	71.81	62.09	43.57			
rc_N75072_at	N75072	2689	EST		3.73	0.00379	5.14	6.21	15.5	104.12	104.99	81.79			
rc_N75120_at	N75120	2690	EST		#N/A	#N/A	20.59	23.42	10.65	61.42	58.88	13.84			
rc_N76086_r_at	N76086	2695	EST		#N/A	#N/A	8.23	7.19	6.54	55.55	55.02	35.47			

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change		metastati c:		metastati c:		normal set 2:		normal set 2:	
			In metas	p value	Median	Mean	Median	Mean	Median	Std Dev	Median	Std Dev
rc_N80129_i_at N87590_at	N80129 N87590	2703 metallothionein 1L EST	66.48 #N/A	0.00415 #N/A	179.8 1.04	104.5 -3.72	9.99 9.99	64.67 64.67	10421.47 59.2	6358.88 35.53	9618.88 35.53	
rc_N91882_at	N91882	2720 alpha2,3-sialyltransferase	14.52	0.00024	-0.18	0.18	34.36	512.3	550.51	320.62		
rc_N93191_at	N93191	2730 EST	3.25	0.00232	174.54	168.53	56.36	659.95	565.08	409.15		
rc_N93403_at	N93403	2734 EST	#N/A	#N/A	4.44	7.63	11.8	48.84	38.39	30.93		
rc_N93470_at	N93470	2736 EST	#N/A	#N/A	14.01	8.69	17.09	77.86	66.84	70.45		
rc_N93764_at	N93764	2737 EST	5.92	0.0109	113.46	68.13	96.98	771.74	792.59	504.88		
N94146_at	N94146	2739 EST	8.05	0	28.92	34.7	14.14	258.82	265.55	101.53		
N99542_at	N99542	2747 orosomucoid 1	8.41	0.00001	6.74	10.14	21.89	226.06	187.68	146.11		
glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease)												
rc_R02365_f_at rc_R05309_f_at	R02365 R05309	2755 2759 EST	17.17 3.72	0.00124 0.0008	0.92 21.94	-5.3 13.92	9.39 18.75	768.72 96.81	444.03 100.54	841.02 31.73		
SEC24 (S. cerevisiae) related gene family, member												
rc_R05490_at	R05490	2761 B	3.03	0.00317	5.87	3.49	12.23	75.28	78.17	48.59		
rc_R06002_s_at	R06002	2763 EST	10.15	0.00003	10.52	8.26	20.8	292.89	264.17	160.28		
rc_R06271_s_at	R06271	2766 EST	6.14	0.00063	23.1	18.95	21.07	208.75	221.65	107.72		
rc_R06273_f_at	R06273	2767 EST	#N/A	#N/A	138	103.77	75.66	235.98	183.78	122.56		
rc_R06543_at	R06543	2769 EST	#N/A	#N/A	61.75	61.42	88.77	163.57	144.04	96.98		
rc_R06746_at	R06746	2771 EST	15.77	0.00009	13.37	-0.9	39.24	455.48	410.16	191.35		
rc_R06860_at	R06860	2773 EST	#N/A	#N/A	84.61	75.89	71.35	104.51	116.59	44.71		

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastati			normal			normal		
			In metas	P value	c: Median	c: Std Dev	c: Mean	c: Std Dev	set 2: Median	set 2: Mean	set 2: Std Dev	set 2: Median	set 2: Mean	set 2: Std Dev
rc_R06977_f_at	R06977	2775 glucokinase (hexokinase 4)	6.1	0.00049	-47.7	-38.97	37.79	152.22	150.69	87.15				
rc_R08564_at	R08564	2780 regulatory protein	60.18	0.00091	69.78	24	105.91	2485.63	2384.62	531.43				
rc_R09053_at	R09053	2783 plasminogen-like	5.9	0.0002	6.45	17.17	35.01	186.87	204.61	113.19				
rc_R10287_at	R10287	2785 EST	11.2	0.0003	7.46	4.94	35.03	376.82	434.91	198.74				
rc_R10684_at	R10684	2788 EST	5.51	0.00741	28.67	1.31	62.39	217.05	221.32	122.94				
rc_R12472_at	R12472	2789 EST	55.18	0.00011	32.21	3.13	76.26	2002.79	1930.03	1097.37				
rc_R12579_at	R12579	2790 EST	3.5	0.00137	54.49	37.84	26.65	198.7	194.59	92.03				
R19808_at	R19808	2796 EST	#N/A	#N/A	9.95	12.2	25.55	27.53	25.43	10.61				
rc_R31104_f_at	R31104	2811 EST	#N/A	#N/A	-6.45	0.74	37.65	32.27	26.77	13.57				
R31641_at	R31641	2814 EST	9.96	0.00011	29.02	21.83	31.18	350.89	330.68	166.29				
rc_R33146_at	R33146	2819 EST	7	0.00043	3.32	2.1	10.76	179.67	195.02	107				
rc_R34362_at	R34362	2822 KIAA0327 gene product	5.4	0.04615	621.7	353.73	689.66	2107.55	2121.04	1000.75				
rc_R39238_at	R39238	2836 synaptosomal 1	#N/A	#N/A	16.06	16.03	9.94	26.8	23.84	16.46				
rc_R40395_s_at	R40395	2841 lecithin-cholesterol acyltransferase	37.33	0.00032	0.98	-46.23	77.82	1192.03	1230.66	281.28				
rc_R40556_s_at	R40556	2843 EST	3.57	0.00184	8.98	8.28	11.75	91.55	95.59	58.66				
rc_R40946_f_at	R40946	2845 crystallin, zeta (quinone reductase)	6.14	0.00156	18.65	19.52	14.3	205.48	220.3	137.27				
rc_R43174_s_at	R43174	2848 paraoxonase 1	74.04	0.00038	47.94	-8.83	119.68	2926.85	3104.07	1318.41				
rc_R43347_at	R43347	2849 carcinoma	#N/A	#N/A	36.93	32.68	30.41	105.66	100.62	28.62				
rc_R43365_at	R43365	2850 EST	5.37	0.00103	5.57	6.67	12.18	150.58	112.8	122.96				
rc_R43910_at	R43910	2852 EST	5.71	0	23.41	24.6	11.1	156.7	166.34	52.21				
rc_R45480_l_at	R45480	2863 cyclin K	#N/A	#N/A	27.21	17.36	21.39	71.04	79.77	50.88				
rc_R49602_at	R49602	2885 EST	36.5	0.00001	19.25	9.65	26.41	970.39	905.54	322.69				
rc_R51831_at	R51831	2891 EST	5.03	0.00761	5.89	2.5	44.67	221.54	195.97	179.99				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in metas			metastat1			normal set 2:			normal set 2:		
			12.79	0.00001	10.78	0.35	28.51	380.07	441.17	180.12	c: Std	Median	Mean	Std Dev
rc_R52822_l_at	R52822	2896 EST	#N/A	#N/A	17.84	25.74	11.45	48.77	44.34	18.43				
rc_R53044_at	R53044	2898 KIAA0981 protein	#N/A	#N/A	9.88	5.59	10.68	66.28	52.16	49.21				
rc_R53891_at	R53891	2900 EST	#N/A	#N/A	34.37	35.83	22.13	94.44	91.55	36.35				
rc_R59312_at	R59312	2913 EST	#N/A	#N/A	19.74	0.00016	18.78	-4.94	51.34	628.69	642.78	316.88		
rc_R59722_at	R59722	2916 EST	#N/A	#N/A	31.21	23.86	17.79	72.94	69.87	45.25				
rc_R60959_at	R60959	2919 EST	#N/A	#N/A	10.83	0.00243	73.01	104.54	56.5	707.38	751.42	357.22		
rc_R62519_f_at	R62519	2926 EST	5.4	0.00202	2.58	9.54	17.4	157.98	128.33	139.55				
rc_R63545_at	R63545	2927 EST												
fatty-acid-Coenzyme A														
rc_R63734_at	R63734	2928 ligase, long-chain 3	#N/A	#N/A	13.28	17.42	12.17	42.74	39.66	18.51				
rc_R64534_at	R64534	2934 EST	#N/A	#N/A	12.11	14.54	5.77	40.32	40.98	17.27				
kynurenine 3-monooxygenase														
rc_R65593_s_at	R65593	2935 (kynurenine 3-hydroxylase)	21.27	0.00007	28.84	18.5	43.46	704.58	812.38	352.86				
rc_R67970_s_at	R67970	2940 gamma-glutamyl carboxylase	9.45	0.00212	85.44	59.33	76.67	655.11	692.66	267.95				
rc_R70319_at	R70319	2946 EST	#N/A	#N/A	5.34	2.91	8.92	29.23	29.18	10.78				
rc_R70791_at	R70791	2949 EST	#N/A	#N/A	127.11	110.15	41.83	73.19	57.2	56.17				
differentially expressed in adenocarcinoma of the lung														
R71459_at	R71459	2953	#N/A	#N/A	16.9	11.46	16.47	37.42	30.98	20.83				
rc_R73468_at	R73468	2957 EST	#N/A	#N/A	9.97	10.43	9.69	38.29	44.82	17.14				
rc_R73816_at	R73816	2961 EST	11.53	0.00259	-26.88	-30.68	10.09	462.31	374.67	450.91				
R77539_at	R77539	2965 EST	#N/A	#N/A	5.91	14.55	25.48	70.5	59.8	31.72				
rc_R78713_s_at	R78713	2968 EST	#N/A	#N/A	0.27	-1.59	8.92	70.57	57.33	56.37				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank	Seq ID	Known Gene Name	fold change in metas			metastat1 c: Std Dev			metastat1 metastat1			normal set 2: set 2:		
				p value	c: Mean	Median	c: Std Dev	Mean	Median	normal Std Dev	normal Std Dev	normal Std Dev	normal Std Dev	normal Std Dev	normal Std Dev
R82229_at	R82229	2975	phosphatidylserine decarboxylase	3.08	0.03455	84.63	80.61	67.01	228.19	232.06	58.38	58.38	58.38	58.38	
rc_R91060_at	R91060	2981	EST	#N/A	59.14	37.15	56.04	85.88	61.99	68.99	68.99	68.99	68.99	68.99	
rc_R93507_at	R93507	2991	EST	#N/A	19.53	20.08	11	67.62	67.56	44.22	44.22	44.22	44.22	44.22	
rc_R93714_at	R93714	2992	fetuin B	10.42	0.00043	-60.74	-65.14	57.99	280.62	301.36	203.86	203.86	203.86	203.86	
rc_R93908_at	R93908	2994	EST	5.8	0.02699	66.75	29.54	129.46	348.58	301.29	173.81	173.81	173.81	173.81	
rc_R94674_s_at	R94674	2996	EST	10.76	0.00008	0.91	4.15	14.66	269.49	288.56	148.06	148.06	148.06	148.06	
rc_R96822_at	R96822	3000	EST	8.25	0.00008	16.45	17.01	30.67	250.81	257.18	131.85	131.85	131.85	131.85	
cytochrome P450, subfamily VIIIIB (sterol 12-alpha-hydroxylase), polypeptide 1															
rc_R97419_at	R97419	3004	EST	65.07	0.0039	152.16	-3.42	302.56	4114.39	3837.4	1458.43	1458.43	1458.43	1458.43	
rc_R97804_at	R97804	3008	EST	#N/A	144.46	187.67	95.8	193.05	201.89	61.84	61.84	61.84	61.84	61.84	
R98073_at	R98073	3009	EST	46.87	0	-4.33	-9.52	11.43	1161.51	1291.95	564.26	564.26	564.26	564.26	
rc_R98105_at	R98105	3011	EST	#N/A	132.16	97.16	141.15	373.83	342.91	215.89	215.89	215.89	215.89	215.89	
rc_R98413_at	R98413	3012	EST	9.71	0.00007	38.74	28.05	21.96	402.49	443.47	212.95	212.95	212.95	212.95	
rc_R98624_at	R98624	3013	EST	21.32	0	15.01	4.48	22.97	686.81	542.22	466.97	466.97	466.97	466.97	
R99014_at	R99014	3015	EST	#N/A	26.99	17.82	29.49	49.82	52.35	18	18	18	18	18	
rc_R99591_at	R99591	3016	CD5 antigen-like (scavenger receptor cysteine rich family)	9.52	0.00006	87.08	72.59	28.25	1035.39	904.92	691.83	691.83	691.83	691.83	
S62539_s_at	S62539	3022	insulin receptor substrate 1	3.7	0.01307	28.26	13.05	40.92	132.59	97.52	103.35	103.35	103.35	103.35	

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	ln metas	P value	fold change	metastati		metastati		normal	
						c: Mean	c: Median	c: Std Dev	c: Std Dev	set 2: Median	set 2: Std Dev
aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase											
S68287_at	S68287	3025_4)	24.11	0	6.23	6.37	9.75	510.59	569.32	165.14	
S69232_at	S69232	3027 flavoprotein dehydrogenase	4.9	0.00017	2.73	4.9	4.29	113.33	103.27	60.93	
S70004_at	S70004	3029 glycogen synthase 2 (liver)	9.96	0.00001	-0.03	-4.28	11.42	225.1	212.32	102.76	
S72370_at	S72370	3030 pyruvate carboxylase	5.31	0.00075	3.83	5.81	23.1	113.03	118.49	50.19	
S77410_at	S77410	3035 angiotensin receptor 1	10.4	0	18.77	17.34	10.85	266.59	284.37	98.14	
S82240_at	S82240	3039 ras homolog gene family, member E	#N/A	#N/A	19.9	6.78	30.8	75.14	74.07	40.43	
T08879_at	T08879	3049 cathepsin F	5.29	0.0008	17.98	14.06	12.92	156.33	180.88	79.67	
rc_T16306_at	T16306	3068 EST	#N/A	#N/A	24.23	23.64	24.91	58.82	63.62	22.35	
protein tyrosine phosphatase type IV, member 1											
rc_T40895_at	T40895	3117 member 1	#N/A	#N/A	1575.59	2039.82	1098.29	4148.86	2440.28	4169.52	
rc_T46901_at	T46901	3123 EST	77.28	0.0006	11.33	-31.1	121.66	2608.54	2853.98	691.43	
rc_T48075_f_at	T48075	3130 hemoglobin, alpha 1	32.56	0.00172	246.19	164.89	271.65	7193.85	5199.28	6317.01	
rc_T50773_s_at	T50773	3136 apolipoprotein C-IV	#N/A	#N/A	94.77	43.61	169.6	8473.97	6484.47	7036.85	

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastati c:			metastati metastati			normal set 2: set 2:		
			In metas	p value	c: Mean	Median	Dev	c: Std	Mean	Median	Dev	Mean	Std Dev	
solute carrier family 22 (extraneuronal monoamine transporter), member 3														
rc_T51617_at	T51617	3138	17.67	0.00018	29.08	19.44	56.17	669.34	725.25	402.58				
rc_T51930_at	T51930	3139	9.99	0.00066	8.27	9.41	5.97	325.48	218.59	298.12				
rc_T56281_f_at	T56281	3151	RNA helicase-related protein	32.34	0.00002	71.16	62.87	44.81	2132.07	2146.52	824.76			
T57140_s_at	T57140	3152	paraoxonase 3	28.8	0	-1.37	-7.55	22.26	825.16	979.66	487.32			
rc_T58756_at	T58756	3156	EST	13.39	0.00013	7.38	-19.91	46.26	390.04	386.76	164.41			
small inducible cytokine subfamily A (Cys-Cys), member 16														
rc_T58775_at	T58775	3157	21.18	0.00006	11.93	-0.59	34.83	577.14	540.96	205.27				
carbamoyl-phosphate synthetase 1, mitochondrial														
rc_T59148_s_at	T59148	3158	88.89	0	17.1	2.26	49.29	3384.09	3845.28	2295.81				
rc_T61256_s_at	T61256	3162	(fructokinase)	13.59	0.00425	55.8	29.78	120.62	752.99	846.1	315.74			
rc_T61654_f_at	T61654	3166	apolipoprotein A-I	#N/A	66.98	-33.89	208.52	9388.4	4297.02	12058.3				
rc_T64933_r_at	T64933	3174	EST	#N/A	1.58	10.35	17.94	52.88	40.46	54.68				
rc_T65443_s_at	T65443	3175	EST	#N/A	10.45	9.99	13.16	70.03	75.01	29				
rc_T66189_s_at	T66189	3178	glutaryl-Coenzyme A dehydrogenase	8.61	0.00003	17.08	20.49	23.82	269.19	301.13	136.96			
rc_T67520_at	T67520	3182	EST	#N/A	52.46	49.25	28.02	105.56	113.95	38.23				
rc_T67705_s_at	T67705	3183	astroglycoprotein receptor 2	31.6	0.00705	168.64	37.91	284.26	2403.76	2437.4	683.22			

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in metas			metastat! c: Std Dev			normal set 2: Median			normal set 2: Std Dev		
			p value	c: Mean	Median	c: Std Dev	Mean	Median	c: Std Dev	Mean	Median	c: Std Dev	Mean	Median
rc_T67931_at	T67931	fibrinogen, B beta polypeptide	49.55	0	-22.74	-22.4	23.54	1187.95	1000.67	692.18				
		short-chain dehydrogenase/reductase 1	4.03	0.01593	65.11	47.59	67.87	263.22	280.22	136.48				
T68083_at	T68083	dehydrogenase EST	3.87	0.00617	0.88	-1.97	11.33	113.31	94.26	103.92				
T68510_at	T68510	EST	37.65	0.00036	19.73	-26.69	95.05	1388.67	1074.67	890.91				
rc_T68711_at	T68711	EST	34.04	0	8.38	6.98	9	800.27	911.26	406.27				
rc_T68855_at	T68855	EST	5.39	0.00383	32.69	17.15	46.31	202.05	208.64	90.02				
rc_T69020_s_at	T69020	EST	4.38	0.00548	34.31	17.81	30.85	173.2	167.2	85.34				
		mannose-binding lectin (protein C)2, soluble (opsonic defect)	36.53	0	9.82	0.32	17.14	1147.2	618.07	972.57				
		#N/A	#N/A	#N/A	-107.09	-119.3	45.51	4052.6	4262.37	3025.26				
T69384_at	T69384	period (Drosophila) homolog	5.88	0.01219	37.94	19.8	90.03	232.84	205.78	126.44				
rc_T71978_at	T71978	EST	4.39	0.0017	41.46	58.86	43.93	218.38	208.73	89.39				
rc_T72171_s_at	T72171	thyroxin-binding globulin	10.41	0.00163	5.48	-20.52	54.58	492.89	371.71	454.89				
rc_T72502_at	T72502	EST	8.87	0.00009	24.11	24.41	28.19	308.87	271.27	179.15				
rc_T72906_at	T72906	EST	7.56	0.00062	4.88	3.04	14.04	233.73	199.26	211.99				
rc_T73442_at	T73442	EST	94.41	0	28.55	25.96	25.95	3170.29	3275.73	1073.74				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastat1			normal			normal		
			In metas	p value	c: Mean	c: Std Dev	c: Median	c: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev
alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)														
rc_T73739_s_at	T73739	3214	16.18	0.00277	1891.22	896.45	2229.6	26094.38	15281.08	25947.4				
rc_T74542_s_at	T74542	3215	32.36	0.00004	27.96	25.04	64.23	1374.78	1445.94	869.3				
rc_T74608_at	T74608	3216	14.03	0	-3.14	-1.78	23.12	360.97	328.7	184.85				
rc_T82323_at	T82323	3231	10.14	0	14.47	5.07	19.91	264.33	229.92	135.46				
T83397_at rc_T84084_at	T83397 T84084	3233 EST	63.6 #N/A	0 #N/A	-17.97 21.47	-4.64 9.96	35.51 68.96	1404.6 66.69	1421.69 605.99	605.99 27.4				
rc_T84491_at rc_T86482_at rc_T87224_at rc_T90037_at rc_T90520_at rc_T91161_at	T84491 T86482 T87224 T90037 T90520 T91161	3235 3238 3241 3246 3249 3253	CUG triplet repeat, RNA-binding protein 2 transferrin EST EST EST EST	#N/A #N/A #N/A 3.99 8.67 3.48	32.84 7.6 451.54 23.17 9.05 9.95	34.93 9.41 184.49 25.82 23.62 2.64	8.15 12.34 184.49 -7.07 25.65 11.55	79.08 316.82 909.33 150.67 306.39 77.85	80.41 197.03 851.86 107.18 362.5 70.8	33.03 302.36 431.47 126.19 204.34 30.28				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID T95813_f_at	Genbank T95813	Seq ID 3262	Known Gene Name KIAA1051 protein	fold change		metastati		metastati		normal	
				In metas	p value	c: Mean	c: Std	c: Median	c: Dev	Median	Std Dev
U00115_at	U00115	3272	B-cell CLL/lymphoma 6 (zinc finger protein 51)	5.18	0.00045	16.17	10.31	26.94	132.13	133.88	32.06
U01120_at	U01120	3274	glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease) (disease)	13.41	0.00147	83.05	45.5	91.8	878.33	693.43	495.6
U02388_at	U02388	3278	cytochrome P450, subfamily IVF, polypeptide 2	9.38	0.00001	-4.93	-3.43	18.14	207.48	207.15	90.12
U03056_at	U03056	3280	hyaluronoglucosaminidase 1	6.64	0	12.68	11.77	4.73	139.32	137.21	43.97
U05861_at	U05861	3285	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	23.22	0.00002	47.98	44.41	21.91	1070.69	962.74	359.01
U06641_s_at U06863_at	U06641 U06863	3287 3288	UDP glycosyltransferase 2 family, polypeptide B15 follistatin-like 1	24.32 3.09	0.00001 0.00091	56.39 43.48	62.92 45.73	54.9 14.83	1762.46 141.97	1615.25 149.4	1206.06 59.45

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in metas			metastati c:			normal set 2: Mean			normal set 2: Median			normal set 2: Std Dev		
			metastati p value	c: Mean	Median	metastati c: Std Dev	Mean	Median	metastati c: Std Dev	Mean	Median	metastati c: Std Dev	Mean	Median	metastati c: Std Dev	Mean	Median
U08006_s_at	U08006	complement component 8, alpha polypeptide	16	0.00111	47.06	31.92	47.52	633.01	661.72	661.72	102.98						
U08198_m1_at	U08198	complement component 8, gamma polypeptide	19.71	0	-29.27	-38.32	47.54	544.28	630.51	630.51	234.87						
U08854_s_at	U08854	UDP glycosyltransferase 2 family, polypeptide B15	7.38	0.00005	10.72	6.45	10.71	181.08	184.97	184.97	91.81						
U11313_at	U11313	sterol carrier protein 2	5.44	0.00187	17.39	0.82	35.86	181.8	228.15	228.15	99.25						
U12778_at	U12778	acyl-Coenzyme A dehydrogenase, short/branched chain	5.68	0.00116	5.23	6.16	7.33	147.06	158.14	158.14	91.5						
U13061_m1_at	U13061	sulfotransferase family 2A, dehydroepiandrosterone (DHEA) -preferring, member 1	11.32	0.00048	9.86	7.49	19.46	369.12	431.45	431.45	213.83						
U15174_at	U15174	BCL2/adenovirus E1B 19kD-interacting protein 3	#N/A	#N/A	41.72	11.86	49.01	129.19	138.02	138.02	68.72						
U15932_at	U15932	dual specificity phosphatase 5	#N/A	#N/A	47.94	27.05	47.87	86.73	86.97	86.97	38.45						
U17989_at	U17989	nuclear autoantigen	#N/A	#N/A	14.21	12.72	6.13	44.22	41.28	41.28	19.09						

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in metas		metastati c:		metastati c: Std Dev		normal set 2: Median		normal set 2: Std Dev	
			p value	c: Mean	Median	Mean	Dev	Median	Mean	Dev	Median	Mean
U19495_s_at	U19495	3319 stromal cell-derived factor 1	4.59	0.00011	7.17	5.76	5.65	103.81	114.61	50.36		
U19523_at	U19523	GTP cyclohydrolase 1 (dopa-responsive dystonia)	5.25	0.00029	12.84	12.26	15.75	136.86	142.71	66.64		
U20530_at	U20530	secreted phosphoprotein 2, 24kD dihydropyrimidine dehydrogenase	16.93	0	12.63	11.54	9.93	383.92	421.24	128.02		
U20938_at	U20938	3324 dehydrogenase	3.92	0.00053	6.66	6.08	7.12	90.66	97.02	44.64		
U22029_f_at	U22029	cytochrome P450, subfamily II A (phenobarbital-inducible), polypeptide 7	71.98	0	5.05	10.11	21.51	1968.7	1339.04	1937.45		
U22662_at	U22662	nuclear receptor subfamily 1, group H, member 3	#N/A	5.71	14.46	20.18	63.21	58.72	37.5			
U31342_at	U31342	#N/A nucleobindin 1	#N/A	77.59	66.2	40.03	183.59	197.29	58.86			
U32576_ma1_at	U32576	apolipoprotein C-IV	18.59	0.00005	311.97	318.75	271.42	1299.4	1145.33	698.02		
U32576_ma1_at	U32576	apolipoprotein C-IV	18.59	0.00005	-7.01	-23.2	62.7	606.88	608.66	224.72		
U32989_at	U32989	tryptophan 2,3-dioxygenase	10.07	0.02825	166.12	22.7	333.99	527.61	473.11	268.8		

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			normal			normal		
			In metas	p value	c: Mean	c: Median	c: Std Dev	c: Mean	c: Median	c: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	
U37055_mna1_s_at	U37055	macrophage stimulating 1 (hepatocyte growth factor-like), macrophage stimulating, pseudogene 9	18.28	0	-7.37	-38.2	47.48	549.49	626.51	217.69				
U37143_at	U37143	cytochrome P450, subfamily IIJ (arachidonic acid epoxidase) polypeptide 2	#N/A	#N/A	33.79	28.24	31.46	116.06	131.46	48.68				
U37547_at	U37547	#N/A	#N/A	29.52	19.51	48.74	93.6	112.45	52.27					
U39226_at	U39226	myosin VIIA (Usher syndrome 1B (autosomal recessive, severe))	#N/A	#N/A	33.54	31.07	8.59	53.24	50.47	20.86				
U46689_at	U46689	aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)	3.5	0.01292	31.22	25.36	49.19	124.41	136.16	53.23				
U48707_at	U48707	protein phosphatase 1, regulatory (inhibitor) subunit 1A	14.22	0	-1.33	-1.45	20.92	319.97	310.24	125.51				
U49082_at	U49082	transporter protein	9.17	0.00088	71.87	46.71	56.13	563.34	515.31	179.82				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastat1 c:			metastat1 c: Std Dev			normal set 2: Median		normal set 2: Std Dev	
			In metas	P value	c: Mean	Median	c: Std Dev	Mean	Median	Std Dev	Mean	Median	Std Dev	Mean	Median
ATP-binding cassette, sub-family C (CFTR/MRP), member 2															
U49248_at	U49248	3374 member 2	7.06	0.00067	30.01	26.03	36.14	231.96	249.25	91.2					
U50929_at	U50929	3380 betaine-homocysteine methyltransferase	36.91	0	8.63	2.82	20.35	898.57	865.9	313.61					
U51010_s_at	U51010	3381 nicotinamide N-methyltransferase	27.79	0.00366	105.25	43.72	204.23	1589.66	1590.62	536.04					
U56814_at	U56814	3393 deoxyribonuclease I-like 3	29.43	0.00003	5.04	11.75	22.3	853.78	1073.24	434.79					
U57094_at	U57094	3394 RAB27A, member RAS oncogene family	#N/A	#N/A	30.85	31.58	23.86	93.06	93.79	50.75					
U59111_at	U59111	3397 dermalan sulphate proteoglycan 3	#N/A	#N/A	32.34	26.73	15.11	68.69	64.44	32.48					
U59423_at	U59423	MAD (mothers against decapentaplegic, Drosophila) homolog 1	#N/A	#N/A	17.46	16.81	10.17	60.5	51.09	37.25					
U60061_at	U60061	3400 fasciculation and elongation protein zeta 2 (zygin II)	#N/A	#N/A	61.44	29.18	68.3	55.02	66.29	38.2					
U66672_at	U66672	3407 ATP-binding cassette, sub-family A (ABC1), member 5	#N/A	#N/A	78.03	41.24	72.76	105.45	97.64	60.15					

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			normal		
			In metas	p value	c: Median	c: Std Dev	c: Mean	set 2: Median	set 2: Mean	set 2: Std Dev	
U68233_at	U68233	nuclear receptor subfamily 1, group H, member 4	6.76	0.00022	19.94	9.8	29.99	198.25	233.6	83.71	
U69141_at	U69141	glutaryl-Coenzyme A dehydrogenase	3.06	0.00053	35.13	27.91	13.89	108.36	119.26	34.82	
U70732_m1_at	U70732	glutamic-pyruvate transaminase (alanine aminotransferase)	27.63	0	-47.95	-65.21	50.88	696.22	732.8	284.7	
U70732_m1_at	U70732	glutamic-pyruvate transaminase (alanine aminotransferase)	27.63	0	-1.44	3.98	66.42	201.88	218.68	136.17	
U72515_at	U72515	putative protein similar to nessy (Drosophila)	#N/A	45.44	58.93	45.12	137.35	138.01	55.38		
U73514_at	U73514	hydroxyacyl-Coenzyme A dehydrogenase, type II	3.79	0.01392	9.85	-22.7	56.91	159.74	161.9	127.8	
U77396_at	U77396	LPS-induced TNF-alpha factor	4.47	0.00108	30.53	33.74	31.54	169.83	141.36	87.43	
U77594_at	U77594	retinoic acid receptor responder (lazarotene induced) 2	11.95	0.00527	94.59	122.86	71.01	838.98	864.02	313.87	
U79716_at	U79716	reelin	3.51	0.00053	14.44	9.15	15.58	90.6	101.49	36.51	
U80226_s_at	U80226	4-aminobutyrate aminotransferase	#N/A	39.69	51.46	20.33	86.94	91.76	24.15		

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in metas	p value	metastat! c: Mean	metastat! c: Median	metastat! c: Std Dev	normal set 2: Mean	normal set 2: Median	normal set 2: Std Dev
U81607_at	U81607	A kinase (PRKA) anchor solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 2	#N/A	#N/A	18.75	8.46	50.91	82.7	78.31	62.79
U82108_s_at	U82108	solute carrier family 31 (copper transporters), member 2	3.19	0.01545	58.61	78.15	43.49	130.34	122.39	73.74
U83461_at U85193_at	U83461 U85193	nuclear factor I/B	#N/A #N/A	#N/A #N/A	24.64 21.84	21.28 23.61	13.16 4.44	51.79 72.71	48.53 68.69	20.85 32.02
U90544_at	U90544	solute carrier family 17 (sodium phosphate), member 2	6.42	0.00023	-3.14	-5.18	19.12	157.41	168.92	63.8
U95090_at	U95090	nephrosis 1, congenital, nephrosis 1, Finnish type (nephrin)	14.01	0.00018	40.49	30.15	38.71	554.93	539.41	183.55
U95090_at W02027_s_at W03796_at rc_W15417_at	U95090 W02027 W03796 rc_W15417	nephrosis 1, congenital, Finnish type (nephrin)	14.01 #N/A 8.3 #N/A	0.00018 #N/A 0.0032 #N/A	4.97 7.28 8.13 30.82	5.87 2.64 -19.16 20.85	18.32 14.09 75.11 38.03	188.83 30.56 336.51 83.24	201.08 28.52 383.56 81.29	88.01 12.47 190.14 49.83
W16686_at	W16686	basic helix-loop-helix domain containing, class B, 2	#N/A	#N/A	46.29	-6.45	123.94	100.9	83.13	78.01

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastati			normal		
			In metas	p value	c: Mean	metastati	c: Std	set 2: Median	set 2: Mean	set 2: Std Dev	
W27503_at	W27503	KIAA0679 protein	#N/A	17.31	21.95	27.71	27.51	5.28			
W28235_at	W28235	EST	#N/A	95.97	81.4	271.36	307.26	108.42			
W28824_at	W28824	EST	15.8	0.00006	-5.59	17.64	441.67	509.29	251		
W36290_s_at	W36290	Kreisler (mouse) maf-related leucine zipper homolog	3.94	0.02718	48.52	10.45	73.21	157.7	156.24	65.15	
W38778_s_at	W38778	EST	#N/A	-55.97	-63.87	44.35	78.01	37.07	137.01		
rc_W42429_at	W42429	EST	#N/A	98.32	80.07	52.23	252.63	300.68	162.35		
rc_W45560_at	W45560	EST	5.06	0.00996	86.81	62.95	81.92	369.61	354.89	158.02	
rc_W48860_at	W48860	EST	#N/A	36.89	39	14.08	52.69	41.31	21.1		
CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II)											
W52581_at	W52581	3543	0.00091	10.92	8.89	10.63	71.35	58.02	37.28		
W58520_at	W58520	3552	#N/A	24.77	26.75	16.56	81.88	87.47	37.77		
rc_W58756_at	W58756	EST	12.17	0.00087	93.37	88.97	71.48	1363.71	1064.26	1032.27	
rc_W60186_at	W60186	EST	3.24	0.00228	19.15	26.5	27.35	101.92	109.68	47.85	
rc_W63741_at	W63741	EST	#N/A	-11.85	-13.73	14.25	28.54	17.1	44.58		
rc_W67147_at	W67147	3568 deleted in liver cancer 1	9.74	0.00002	16.09	9.11	24.66	282.59	235.29	169.33	
rc_W67199_at	W67199	EST	3.09	0.01528	30.05	35	12.16	123.27	117.99	90.47	
rc_W70131_at	W70131	EST	#N/A	#N/A	108.21	30.68	183.05	118.49	100.66	53.4	
rc_W72044_at	W72044	3580 insulin induced gene 1	24.58	0.00001	41.6	36.28	36.46	1133.09	940.16	723.6	
rc_W72079_at	W72079	EST	6.36	0.00641	46.78	17.94	66.71	261.7	214.62	175.87	

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			normal			normal		
			In metas	p value	c: Std Dev	c: Mean	Median	c: Std Dev	Mean	Median	c: Std Dev	Mean	Median	c: Std Dev
oxidative 3 alpha hydroxysteroid dehydrogenase; retinol dehydrogenase														
rc_W72382_at	W72382	3584	dehydrogenase	#N/A	37.21	6.21	66.91	3403.46	3255.54	1538.23				
rc_W72471_at	W72471	3585	EST	#N/A	17.93	13.32	10.61	71.51	76.9	29.33				
rc_W72972_at	W72972	3587	EST	5.61	0.00939	44.7	26.44	80.59	277.4	270.63	183.07			
rc_W73382_at	W73382	3591	EST	#N/A	62.97	39.05	67.26	87.32	89.49	28.17				
rc_W79422_s_at	W79422	3604	fumarylacetateoacetate	14.94	0.00059	-18.4	-19.27	33.52	467.37	_554.19	306.71			
W81053_at	W81053	3610	EST	4.91	0.00164	-21.38	-13.04	24.17	135.84	109.34	113.36			
rc_W85765_at	W85765	3618	EST	3.83	0.00379	3.6	1.46	7.87	108.99	77.01	109.58			
rc_W85847_at	W85847	3619	EST	7.28	0.00024	4.15	5.29	9.26	187.31	160.02	130.73			
rc_W85886_at	W85886	3621	EST	3.46	0.00814	-6.09	-2.4	11.46	99.92	68.44	97.4			
protein C inhibitor (plasminogen activator inhibitor III)														
rc_W86431_s_at	W86431	3627	inhibitor III)	14.94	0.00152	3.16	5.55	12.03	606.44	395.34	590.7			
rc_W86600_at	W86600	3628	EST	32.14	0	12.67	7.49	15.61	792.37	807.74	313.83			
homogenitase 1,2-dioxygenase (homogenitase oxidase)														
rc_W87454_at	W87454	3632	oxidase)	7.93	0.00149	11.36	5.83	39.02	336.07	275.03	315.24			
rc_W87480_at	W87480	3633	STAT Induced STAT Inhibitor-2	3.24	0.01063	31.91	26.07	30.44	129.06	119.73	80.94			
rc_W87606_s_at	W87606	3635	protein Z, vitamin K-dependent plasma glycoprotein	9.23	0.00085	2.53	-1.74	9.98	268.59	280.44	184.7			
rc_W88946_at	W88946	3639	putative glycine-N-acyltransferase	58.26	0	2.16	-22.13	39.9	1717.54	1821.77	502.55			
rc_W90018_f_at	W90018	3642	EST	#N/A	#N/A	-2.1	4.12	13.16	59.32	53.19	41.68			

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change		metastat! c:		metastat! metastat!		normal set 2: c: Std Dev		normal set 2: Median Std Dev	
			In metas	p value	c: Mean	Median	Metastat!	Metastat!	Mean	Median	Mean	Median
<i>cytochrome P450, subfamily IIID (debrisoquine, sparteine, etc., -metabolising), polypeptide 7a (pseudogene)</i>												
X07619_s_at	X07619		4.96	0.00004	32.26	33.56	10.88	177.56	206.15	206.15	77.69	
X07732_at	X07732	hepsin (transmembrane protease, serine 1)	28.21	0	-8.34	-12	39.24	678.15	672.42	672.42	183.61	
X07767_at X12662_ma1_at	X07767 X12662	protein kinase, cAMP-dependent, catalytic, alpha arginase, liver	5.94 20.59	0.00028 0	16.15 11.33	19.43 10.15	11.48 12.81	152.58 486.71	160.88 479.11	160.88 479.11	73.73 199.71	
X13227_at	X13227	D-amino-acid oxidase	4.81	0.0002	25.1	33.95	26.2	166.22	147.21	147.21	77.49	
<i>cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6</i>												
X13930_f_at X14787_at	X13930 X14787	thrombospondin 1	38.52 3.69	0 0.01115	52.66 21.81	64.02 22.87	31.42 7.7	2408.66 143.24	1948.18 86.81	1948.18 86.81	1843.46 166.32	
<i>acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)</i>												
X14813_at X15393_ma1_at	X14813 X15393	motilin	11.61 #N/A	0.0002 #N/A	59.4 70.16	71.51 55.83	42.45 27.07	712.58 113.93	704.45 117.96	704.45 117.96	258.91 26.14	

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	ln metas	p value	fold change		metastati		metastati		normal		
					c: In metas	c: p value	c: Mean	c: Median	c: Std Dev	set 2: Mean	set 2: Median	set 2: Std Dev	
mannose-binding lectin (protein C) 2, soluble (opsonic defect)													
X15422_at	X15422	3708	0.00015	8.29	2.28	2.69	7.25	208.25	221.14	123.22			
X16260_s_at	X16260	3710	0.00933	44.65	40.4	36.54	67	1261.99	1133	523.31			
X16323_at	X16323	3711	#N/A	#N/A	10.65	6.56	6.59	32.58	30.52	9.66			
X16663_at	X16663	3714	Lyn substrate 1	#N/A	48.32	28.69	56.44	81.51	83.53	33.75			
paired basic amino acid cleaving enzyme (furin, membrane associated)													
X17094_at	X17094	3717	receptor protein)	8.5	0	-1.85	7.01	25.41	190.11	216.35	74.11		
alanine-glyoxylate aminotransferase (oxalosis; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)													
X53414_at	X53414	3728	0.00003	13.87	138.92	110.29	90.59	1856.57	1888.79	846.06			
X54380_at	X54380	3730	pregnancy-zone protein	8.44	0.00059	4.93	3.19	19.26	274.41	255.4	203.47		

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change			metastatic			metastatic			normal			normal		
			In metas	p value	c: Mean	metastati	c:	metastati	c: Std Dev	set 2: Median	set 2: Mean	set 2: Std Dev	set 2: Median	set 2: Mean	set 2: Std Dev		
X56411_mna1_at	X56411	alcohol dehydrogenase 4 (class II), pi polypeptide	25.14	0.00144	55.53	11.29	102.45	991.98	943.64	448.31							
X57025_at	X57025	insulin-like growth factor 1 (somatomedin C)	4.72	0.00087	5.88	10.95	10.22	120.82	100.54	85.16							
X60673_s_at	X60673	adenylyl kinase 3	8.3	0.00016	23.02	32.17	44.24	331.58	324.75	164.03							
X63359_at	X63359	UDP glycosyltransferase 2 family, polypeptide B10 c-myc promoter-binding protein	13.66	0.00051	55.28	48.57	41.25	669.93	732.6	161.42							
X63417_at	X63417	#N/A	#N/A	#N/A	#N/A	28.85	27.75	24.56	68.08	56.34	33.18						
X64877_at	X64877	H factor (complement)-like 3	14.6	0	14.6	7.51	21.01	387.8	402.85	151.23							
X64877_s_at	X64877	H factor (complement)-like 3	12.33	0	6.14	8.26	14.25	262.65	268.29	84.84							
X65727_cds2_s_at	X65727	glutathione S-transferase A2,glutathione S-transferase	73.64	0	21.03	17.39	15.18	2162.22	2183.18	1435.52							
X65962_s_at	X65962	cytochrome P450, subfamily IIIC (mephenytoin 4-hydroxylase)	5.47	0.00014	36.73	31.48	11.66	247.79	149.39	208.59							
X76105_at	X76105	death-associated protein	3.02	0.00944	30.12	33.72	31.36	108.68	118.36	56.75							

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in metas	p value	metastati		metastati		normal		normal	
					c: Mean	c: Std Dev	c: Median	c: Std Dev	set 2: Mean	set 2: Std Dev	set 2: Median	set 2: Std Dev
X78992_at	X78992	butyrate response factor 2 (EGF-response factor 2)	4.69	0.01995	64.86	31.76	66.31	318.26	336.95	207.43		
X79981_at	X79981	cadherin 5, VE-cadherin (vascular epithelium)	#N/A	#N/A	45.01	41.07	11.65	80.92	80.1	8.57		
X86401_s_at	X86401	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	22.7	0	19.17	9.16	19.13	646	721.34	274.64		
X90999_at	X90999	hydroxyacyl glutathione hydrolase; glyoxalase 2	5.27	0.00047	16.15	26.83	26.47	170.37	179.54	76.98		
X91148_at	X91148	microsomal triglyceride transfer protein (large polypeptide, 88kD)	5.91	0.00045	15.37	3.85	31.49	173.77	189.11	83.82		
X92396_at	X92396	#N/A	#N/A	#N/A	40.87	17.73	57.17	67.49	61.23	31.24		
X92475_at	X92475	synaptobrevin-like 1 ITBA1 gene	#N/A	#N/A	56.74	63.84	25.6	66.2	63.72	20.36		
X94563_xp12_r_at	X94563	EST	3.52	0.00928	76.79	66.4	52.64	274.91	244.92	177.63		
X95190_at	X95190	acyl-Coenzyme A oxidase 2, branched chain	12.81	0	-80.53	-76.73	37.81	285.88	349.39	119.31		
X97160_ma1_at	X97160	transcription factor binding to IGHM enhancer 3	#N/A	#N/A	61.31	49.54	30.41	75.26	66.36	29.46		

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Afly ID	Genbank Seq ID	Known Gene Name	fold change in metas			metastati c: Median			normal set 2: Mean			normal set 2: Median		
			p value	c: Mean	c: Std Dev	metastati c: Median	c: Std Dev	metastati c: Mean	c: Std Dev	metastati c: Median	c: Std Dev	metastati c: Mean	c: Std Dev	metastati c: Median
complement factor H related 3, complement factor H-related 4														
X98337_s_at	X98337	3840 related 4	13.5	0.00001	18.76	22.2	33.33	411.51	375.08	169.37	39.99			
Y00097_s_at	Y00097	3844 annexin A6	3.4	0.00233	19.43	16.39	33.67	105.39	104.75					
UDP glycosyltransferase 2 family, polypeptide B4														
Y00317_at	Y00317	3845	18.34	0.00001	-9.82	-11.91	20.96	456.09	477.28	257.07				
UDP glycosyltransferase 2 family, polypeptide B4														
Y00317_at	Y00317	3845	18.34	0.00001	11.31	14.85	7.33	231.32	282.35	122.76				
Y00339_s_at	Y00339	3847 carbonic anhydrase II, Interleukin 13 receptor, alpha 1	6.89	0	6.23	-1.39	18.22	168.76	178.44	69.52				
Y10659_at	Y10659	3859 interleukin 13 receptor, alpha 1	4.22	0.00061	18.27	12.85	25.15	123.23	134.47	49.24				
Y10659_at	Y10659	3859 interleukin 13 receptor, alpha 1	4.22	0.00061	15.82	16.3	16.79	81.75	89.09	37.01				
Y12711_at	Y12711	3861 progesterone binding protein	14.83	0.00285	26.37	16.12	99.79	1061.83	935.43	829.85				
aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)														
Z28339_at	Z28339	3875	24.66	0	3.67	3.48	5.1	527.72	552.17	156.66				
Z29481_at	Z29481	3877 3-hydroxyanthranilate 3,4-dioxygenase	6.39	0.00029	546.48	440.33	293.12	2012.12	1797.38	944.18				

Table 9B. Genes and ESTs expressed only in normal liver tissue compared to metastatic liver tissue.

Affy ID	Genbank Seq ID	Known Gene Name	fold change in metas		p value	metastatic c: Median		metastatic c: Std Dev		normal set 2: Median		normal set 2: Std Dev	
			fold	change		metastatic c: Mean	metastatic c: Std Dev	normal set 2: Mean	normal set 2: Std Dev	normal set 2: Median	normal set 2: Std Dev		
Z30425_at	Z30425	nuclear receptor subfamily 1, group I, member 3	26.64	0	5.66	7.49	8.02	181.6	192.48	76.65	76.65		
rc_Z38161_at	Z38161	EST	4.38	0.0011	11.84	12.14	6.32	111.16	107.62	80.11	80.11		
rc_Z38192_s_at	Z38192	EST	3.35	0.00184	-0.28	-4.75	17.86	87.12	87.23	52.58	52.58		
rc_Z38910_at	Z38910	EST	#N/A	#N/A	0.68	2.75	12.7	35.49	32.21	23.55	23.55		
rc_Z39394_at	Z39394	EST	#N/A	#N/A	10.11	10.43	11.1	24.06	22.96	11.11	11.11		
rc_Z39622_s_at	Z39622	EST	4.4	0.00001	19.65	21.87	11.97	110.87	115.21	36.19	36.19		
rc_Z39833_at	Z39833	GTP-binding protein	16.89	0.00034	35.79	41.07	84.59	957.61	1080.1	674.72	674.72		
rc_Z39976_at	Z39976	EST	5.76	0.00012	13.09	7.15	18.64	165.45	151.05	98.9	98.9		
rc_Z40259_s_at	Z40259	EST	8.18	0.00002	14.39	8.61	11.98	218.4	223.24	122.06	122.06		
rc_Z41271_s_at	Z41271	ariadne, Drosophila, homolog of	#N/A	#N/A	51.96	64.49	36.28	145.09	126.18	57.57	57.57		
rc_Z41356_at	Z41356	EST	#N/A	#N/A	4.46	15.94	28.44	82.7	48.14	71.73	71.73		
rc_Z41634_at	Z41634	EST	#N/A	#N/A	16.4	16.07	3	51.19	48.49	33	33		
Z47553_at	Z47553	flavin containing monooxygenase 5	6.17	0.00011	4.86	1.26	8.96	141.98	165.57	59.33	59.33		
Z48054_at	Z48054	peroxisome receptor 1	#N/A	#N/A	46.89	51.87	23.55	78.16	80.88	26.87	26.87		
Z48475_at	Z48475	glucokinase (hexokinase 4) regulatory protein	13.84	0	-42.61	-53.52	23.46	305.23	239.52	155.98	155.98		
Z48633_at	Z48633	EST	#N/A	#N/A	-5.51	-6.39	13.15	36.84	40.63	26.33	26.33		
Z49269_at	Z49269	small inducible cytokine subfamily A (Cys-Cys), member 14	18.46	0.00001	1.88	-25.63	41.94	526.13	532.29	166.67	166.67		
Z49878_at	Z49878	guanidinoacetate N-methyltransferase	13.96	0.00021	44.63	45.34	41.76	615.57	659.09	196.31	196.31		

What is claimed is:

1. A method of diagnosing liver cancer in a patient, comprising:
 - (a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of liver cancer.
2. A method of detecting the progression of liver cancer in a patient, comprising:
 - (a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of liver cancer progression.
3. A method of monitoring the treatment of a patient with liver cancer, comprising:
 - (a) administering a pharmaceutical composition to the patient;
 - (b) preparing a gene expression profile from a cell or tissue sample from the patient; and
 - (c) comparing the patient gene expression profile to a gene expression from a cell population selected from the group consisting of normal liver cells, hepatocellular carcinoma and metastatic liver carcinoma.
4. A method of treating a patient with liver cancer, comprising:
 - (a) administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9;
 - (b) preparing a gene expression profile from a cell or tissue sample from the patient comprising tumor cells; and
 - (c) comparing the patient expression profile to a gene expression profile selected from the group consisting of normal liver cells, hepatocellular carcinoma and metastatic liver carcinoma
5. A method of diagnosing hepatocellular carcinoma in a patient, comprising:

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(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma.

5 6. A method of detecting the progression of hepatocellular carcinoma in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma progression.

10

7. A method of monitoring the treatment of a patient with hepatocellular carcinoma, comprising:

- (a) administering a pharmaceutical composition to the patient;
- (b) preparing a gene expression profile from a cell or tissue sample from the patient; and
- (c) comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising hepatocellular carcinoma cells or to both.

20 8. A method of treating a patient with hepatocellular carcinoma, comprising:

- (a) administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9;
- (b) preparing a gene expression profile from a cell or tissue sample from the patient comprising hepatocellular carcinoma cells; and
- (c) comparing the patient expression profile to a gene expression profile from an untreated cell population comprising hepatocellular cells.

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9. A method of diagnosing a metastatic liver tumor in a patient, comprising:
(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of metastatic liver cancer.

5

10. A method of detecting the progression of a metastatic liver cancer in a patient, comprising:
(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of a metastatic liver cancer progression.

11. A method of monitoring the treatment of a patient with a metastatic liver cancer, comprising:

(a) administering a pharmaceutical composition to the patient;
15 (b) preparing a gene expression profile from a cell or tissue sample from the patient; and
(c) comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising metastatic liver tumor cells or to both.

20

12. A method of treating a patient with a metastatic liver tumor, comprising:
(a) administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9;
25 (b) preparing a gene expression profile from a cell or tissue sample from the patient comprising metastatic liver tumor cells; and
(c) comparing the patient expression profile to a gene expression profile from an untreated cell population comprising metastatic liver tumor cells.

30 13. A method of differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of metastatic liver cancer rather than hepatocellular carcinoma.

5 14. A method of screening for an agent capable of modulating the onset or progression of liver cancer, comprising:

(a) preparing a first gene expression profile of a cell population comprising liver cancer cells, wherein the expression profile determines the expression level of one or more genes from Tables 3-9 ;

10 (b) exposing the cell population to the agent;

(c) preparing second gene expression profile of the agent-exposed cell population; and

(d) comparing the first and second gene expression profiles.

15 15. The method of claim 14, wherein the liver cancer is a hepatocellular carcinoma.

16. The method of claim 14, wherein the liver cancer is a metastatic liver cancer.

20 17. A composition comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 3-9 .

18. A composition according to claim 17, wherein the composition comprises at least 3 oligonucleotides.

25

19. A composition according to claim 17, wherein the composition comprises at least 5 oligonucleotides.

30

20. A composition according to claim 17, wherein the composition comprises at least 7 oligonucleotides.

21. A composition according to claim 17, wherein the composition comprises at least 10 oligonucleotides.

22. A composition according to any one of claims 17-21, wherein the 5 oligonucleotides are attached to a solid support.

23. A composition according to claim 22, wherein the solid support is selected from a group consisting of a membrane, a glass support, a filter, a tissue culture dish, a polymeric material, a bead and a silica support.

10

24. A solid support comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 3-9.

15

25. A solid support according to claim 24, wherein the oligonucleotides are covalently attached to the solid support.

26. A solid support according to claim 24, wherein the oligonucleotides are non-covalently attached to the solid support.

20

27. A solid support according to claim 24, wherein the support comprises at least about 10 different oligonucleotides in discrete locations per square centimeter.

28. A solid support according to claim 24, wherein the support comprises at least about 100 different oligonucleotides in discrete locations per square centimeter.

25

29. A solid support according to claim 24, wherein the support comprises at least about 1000 different oligonucleotides in discrete locations per square centimeter.

30

30. A solid support according to claim 24, wherein the support comprises at least about 10,000 different oligonucleotides in discrete locations per square centimeter.

31. A computer system comprising:

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- (a) a database containing information identifying the expression level in liver tissue of a set of genes comprising at least two genes in Tables 3-9 ; and
(b) a user interface to view the information.

5 32. A computer system of claim 31, wherein the database further comprises sequence information for the genes.

10 33. A computer system of claim 31, wherein the database further comprises information identifying the expression level for the set of genes in normal liver tissue.

15 34. A computer system of claim 31, wherein the database further comprises information identifying the expression level of the set of genes in liver cancer tissue.

20 35. A computer system of claim 34, wherein the liver cancer tissue comprises hepatocellular carcinoma cells.

25 36. A computer system of claim 34, wherein the liver cancer tissue comprises metastatic liver cancer cells.

30 37. A computer system of any of claims 31-36, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.

35 38. A computer system of claim 37, wherein the external database is GenBank.

40 39. A method of using a computer system of any one of claims 31-36 to present information identifying the expression level in a tissue or cell of at least one gene in Tables 3-9, comprising:

45 (a) comparing the expression level of at least one gene in Tables 3, 4, 5, 6, 8 or 3-9 in the tissue or cell to the level of expression of the gene in the database.

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40. A method of claim 39, wherein the expression level of at least two genes are compared.
41. A method of claim 39, wherein the expression level of at least five genes are
5 compared.
42. A method of claim 39, wherein the expression level of at least ten genes are compared.
- 10 43. A method of claim 39, further comprising displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level in liver cancer.

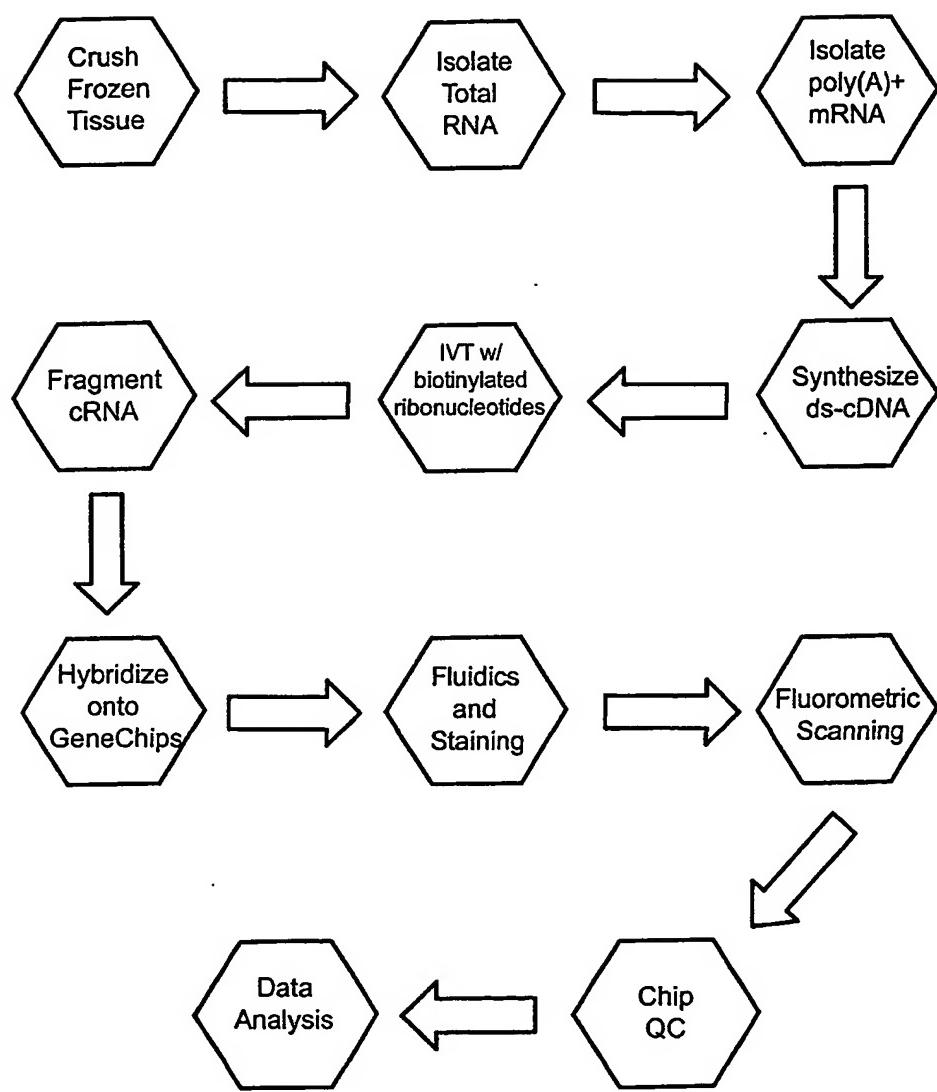
FIGURE 1

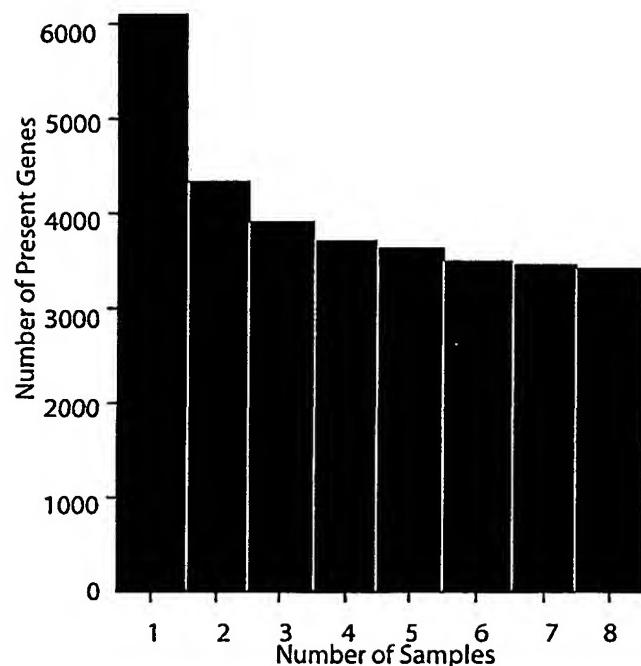
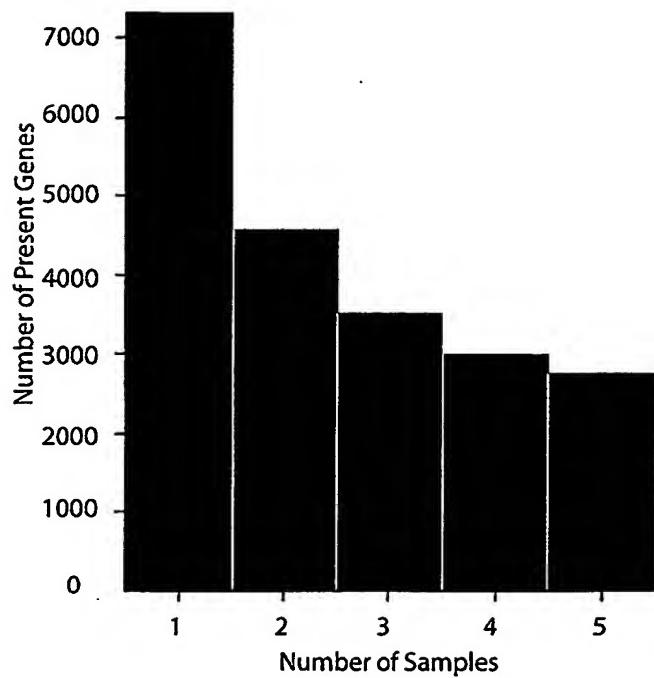
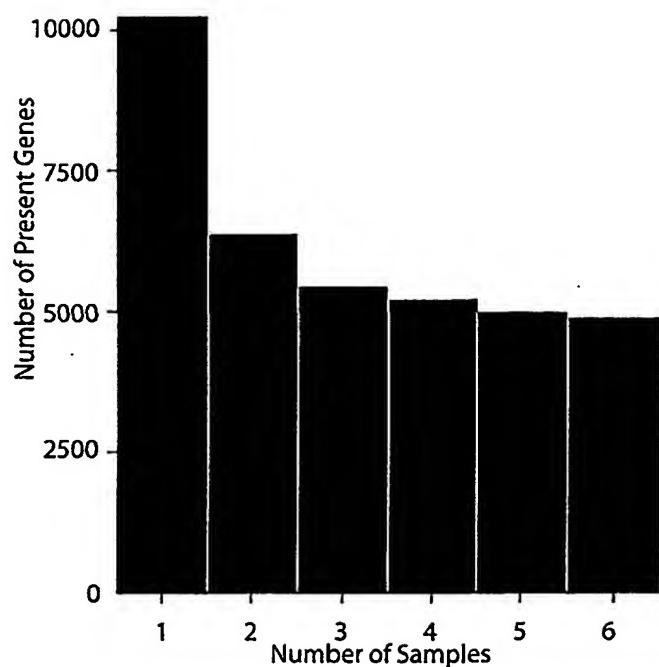
FIGURE 2A

FIGURE 2B

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FIGURE 2C

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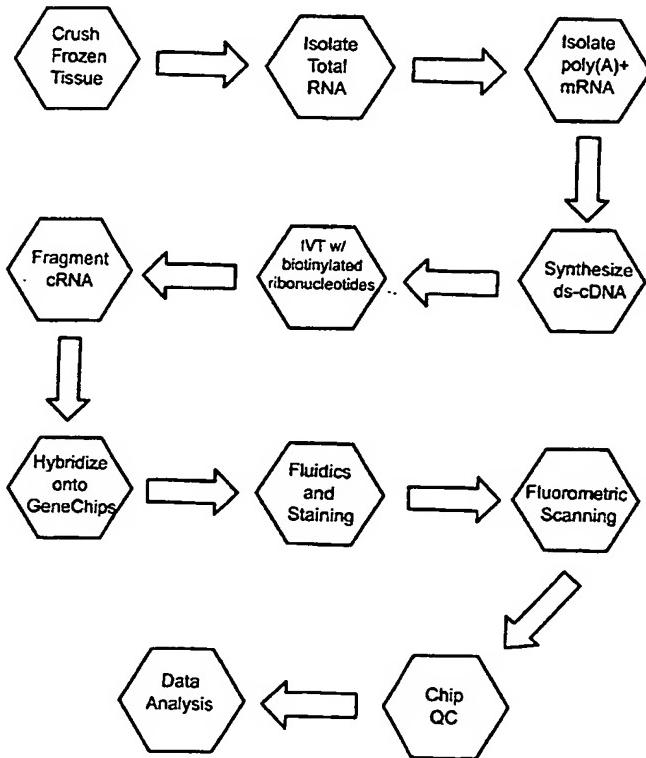
[US/US]; 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). ALVARES, Christopher [US/US]; 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). PERES-DA-SILVA, Supriya [US/US]; 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). VOCKLEY, Joseph, G. [US/US]; 708 Quince Orchard Road, Gaithersburg, MD 20878 (US).

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[Continued on next page]

(54) Title: GENE EXPRESSION PROFILES IN LIVER CANCER



(57) Abstract: The present invention identifies the global changes in gene expression associated with liver cancer by examining gene expression in tissue from normal liver, metastatic malignant liver and hepatocellular carcinoma. The present invention also identifies expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

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INTERNATIONAL SEARCH REPORT

Internal Application No

PCT/US 01/30589

A. CLASSIFICATION OF SUBJECT MATTER
 IPC 7 C12Q1/68 G06F19/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 13334 A (DEUTSCHES KREBSFORSCH ;NEHRBASS DIRK (DE); BANNASCH PETER (DE); KL) 18 March 1999 (1999-03-18) see whole doc. esp. claims e.g. 6	1-43
X	EP 0 857 780 A (SUMITOMO ELECTRIC INDUSTRIES) 12 August 1998 (1998-08-12) see whole doc. esp. claims and p.2, 1.55ff. -/-	1-43

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents :

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- *&* document member of the same patent family

Date of the actual completion of the international search

10 January 2003

Date of mailing of the international search report

12.05.03

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Mueller, F

INTERNATIONAL SEARCH REPORT

Internati	Application No
PCT/US 01/30589	

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DARABI A ET AL: "DIFFERENTIAL GENE EXPRESSION IN EXPERIMENTAL HEPATOCELLULAR CARCINOMA INDUCED BY WOODCHUCK HEPATITIS B VIRUS" CANCER LETTERS, NEW YORK, NY, US, vol. 95, no. 1-2, 1995, pages 153-159, XP000978529 ISSN: 0304-3835 the whole document _____	1-43
X	WO 99 39200 A (UNIV JEFFERSON ;FEITELSON MARK A (US)) 5 August 1999 (1999-08-05) see whole doc. esp. claims and table 1 page 10, _____	1-43

INTERNATIONAL SEARCH REPORT

Inte: national application No.
PCT/US 01/30589

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
see FURTHER INFORMATION sheet PCT/ISA/210
2. Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
claims 1-43 (partially)

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US 01 A0589

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

Although claim(s) 1,2 as far as an in vivo method is concerned are directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition. Although claims 3-14 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US 01 80589

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: INVENTION 1 claims 1-43 (partially)

method of diagnosing liver cancer by detecting expression of gene collagen, type v, alpha and subject-matter as defined by the wording of claims 1-43 restricted to the mentioned gene sequence (Genbank AA055896)

2. Claims: INVENTION 2-3953 claims 1-43 (partially)

ibid. for sequences listed in tables 3-9 for each sequence separately

INTERNATIONAL SEARCH REPORT

Information on patent family members

Internat'l Application No
PCT/US 01/30589

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO 9913334 A	18-03-1999	DE	19739360 A	01-04-1999
EP 0857780 A	12-08-1998	WO	9710333 A	20-03-1997
WO 9939200 A	05-08-1999	AU	2480799 A	16-08-1999

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